Standards for Tree Improvement in Alberta

Land and Forest Division
Alberta Sustainable Resource Development
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PREAMBLE

This manual states standards for Tree (primarily *Spruce, Pine, Aspen, Poplar*) Improvement in Alberta. Use of Genetically Modified Organisms (GMOs) is not approved for reforestation of Provincial Crown land at this time. Federal legislation controls the testing of GMO's, though Alberta may refuse testing on Crown Land if risks are deemed unacceptable.

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GENERAL

1.0 Principles

The forest genetic resources of Alberta are crucial to the well being of the people of Alberta, to sustainable forest management, and to the long-term economic and ecological stability of the province.

The government of Alberta and the forest industry:

- endeavor to ensure the adaptability, diversity and health of *wild* and managed populations, and to conserve the genetic integrity of *wild* populations of trees on the landscape, and
- recognize the value of tree improvement in enhancing the productivity of the forest landbase and generating economic benefit.

Forest managers have responsibilities for maintaining the value of the genetic resources of the province.

The role of government is to:

- protect the public interest and conserve the forest genetic resource by implementing conservation programs and enacting and enforcing policies, regulations and standards,
- promote development of that resource for the economic benefit of the people of Alberta, and
- participate in the development and implementation of tree improvement and related technologies.

The role of the industry is to:

- respect the public interest by conforming to enacted policies, regulations and standards, and
- develop objectives and strategies that will increase the value derived from the forest genetic resource.

2.0 Development and Review of the Standards

Management and conservation standards were developed through extensive consultation with geneticists and other scientific and management professionals. These standards will be adapted to evolving knowledge. They will be formally reviewed annually for the first two years, and again after five years.

The *Alberta Forest Legacy* document guided development of the standards.

3.0 Applicability

These standards apply to the *Green Area*. In addition, the standards for Material Collection, Handling, Registration and Storage apply to all material collected from *public land* as well as all material intended for *deployment* on the *Green Area*, regardless of where the material is collected.

The two main users of the standards are those who:

- work primarily with *wild* material collected for normal *reforestation* activities (*Stream 1*), and
- have *controlled parentage programs* (*Stream 2*).

Genetically Modified Organisms (GMO's)

GMO, or genetically modified organism, refers to an organism that, through human intervention in a laboratory, has had its genome, or genetic code, deliberately altered through the mechanical insertion of a specific identified sequence of genetic coding material (generally DNA) that has been either manufactured or physically excised from the genome of another organism. Genetic modification may be used to alter any of a wide range of traits, including insect and disease resistance, herbicide tolerance, tissue composition, and growth rate.

Though it is recognized that GMO tree material has a theoretical potential for reforestation, the performance and impacts on the forest ecosystem are poorly understood. In view of the potential risks associated with reforestation with GMO trees, and in accordance with the current position of *the Alberta Forest Genetics Council*, GMOs are not approved for use on Crown land in Alberta at this time. The federal government has jurisdiction over testing and use of GMO's in Canada. As such, proponents should contact the appropriate federal department prior to undertaking a program of testing of GMO's. If federal approval for testing of GMO's is granted, this manual outlines additional technical requirements for review, testing, and research from a provincial perspective.

Submission and Approval of Documents

Plans and forms that are required to be submitted to the Department of Sustainable Resource Development (hereinafter referred to as "the Department") as specified in the standards and appendices will receive one of four responses:

1. Approve
2. Approve with conditions
3. Requires additional information
4. Reject with reasons

4.0 Structure of the Document

Following this General information section are five sections containing goals and standards. **Goal** statements describe the intent and scope within each area. **Standards** are the specific results that must be attained, or in some cases specific procedures that must be followed.

The five sections are:

- Ownership and Data Access (ODA),
- Material Collection, Handling, Registration and Storage (MCHRS),
- Green Area Deployment (GAD),
- Breeding, Testing and Verification (BTV), and
- Production of Controlled Parentage Materials (PCPM).

This document also contains a glossary, a list of acronyms and numerous appendices (tables, forms and other supplements to the standards). The glossary provides definitions of terms specific to their usage in this policy.

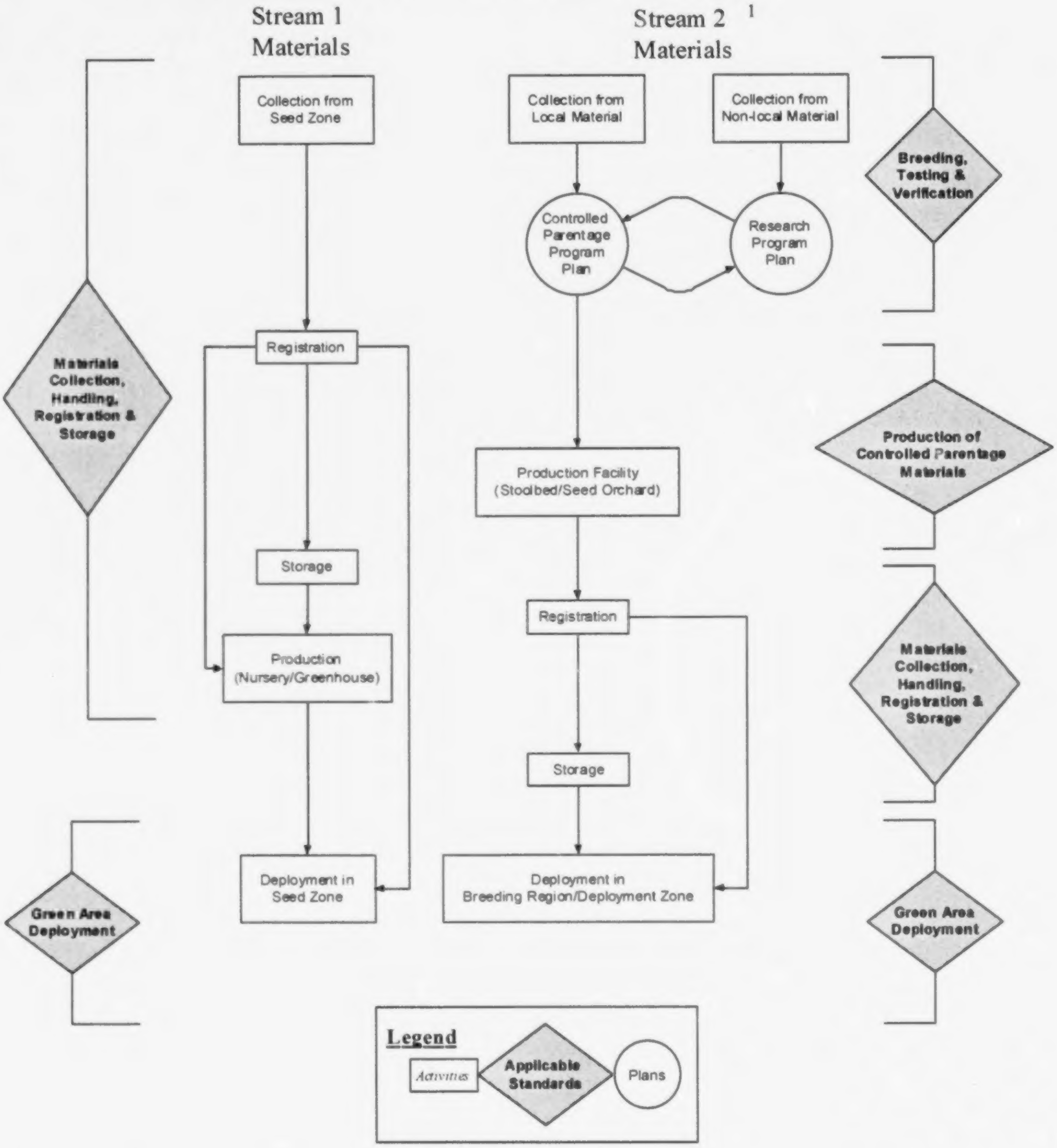
Two notes about the **format** of this document:

1. To help separate which standards apply to each of the two streams of material, a **double-lined box** has been placed around standards that apply **exclusively** to the controlled parentage programs (see Figure 1, *Stream 2*) or research programs. Standards appearing outside the box may apply to both streams of material.
2. Terms found in the glossary appear in **italics** in the text to indicate that the use of the term has been defined.

5.0 Standards Framework

Figure 1 below illustrates a functional arrangement of the components of the Standards for Tree Improvement in Alberta. *Stream 1 material* refers to the adapted seed or vegetative material collected from *wild* or artificially regenerated stands of native species. *Stream 2 material* is that which results from a *controlled parentage program.*

Figure 1: Schematic Representation of Paths to Deployment


Stream 1 Materials
Stream 2 Materials [1]
Collection from Seed Zone
Collection from Local Material
Collection from Non-local Material
Controlled Parentage Program Plan
Research Program Plan
Breeding, Testing & Verification
Materials Collection, Handling, Registration & Storage
Registration
Production Facility (Stoolbed/Seed Orchard)
Production of Controlled Parentage Materials
Storage
Production (Nursery/Greenhouse)
Registration
Materials Collection, Handling, Registration & Storage
Storage
Green Area Deployment
Deployment in Seed Zone
Deployment in Breeding Region/Deployment Zone
Green Area Deployment
Legend
Activities
Applicable Standards
Plans

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[1] See Appendix 1.

6.0 Effective Date and Retroactivity

These standards are enabled through Timber Management Regulation 144.2 and are effective as of May 01, 2003.

Controlled Parentage and Research Programs that already existed or were under development prior to the effective date will be implemented or upgraded to the new standards through discussion with the Department and the proponent(s). The intent is to capitalize on work in progress while phasing in new standards.

OWNERSHIP AND DATA ACCESS (ODA)

Preamble

The Department has stewardship responsibility for the management of forest genetic resources on *public land* in Alberta.

The Department, the forest industry, research organizations and tree improvement cooperatives:

- undertake research, conservation, tree improvement and breeding programs jointly or individually, and
- are involved in the collection and *deployment* of genetically improved trees on *public land* in Alberta.

As tree improvement programs in the province mature, information will accrue on the performance of genetically improved material. The value of such material, and ownership issues, will become of greater importance to government and industry. It is also possible that forest material collected from Alberta *public land* could be utilized for commercial purposes other than fibre production in Alberta. In such instances, benefits to the province must be retained.

Goals

The goals of this section are to:

- establish ownership and access rights to forest genetic resources, and
- state the Department's requirements for access to data on genetically improved forest material to ensure stewardship of Alberta's forested *public land*.

If these standards conflict with copyright, patent and/or intellectual property laws, or other federal laws, such legislation would supersede these standards.

ODA Standards

7.0 Ownership of Material

Trees and tree material (physical tree material) on *public land* are the property of the province. This includes source materials (e.g. pollen, seed, graft materials and vegetative propagules) that have potential for collection through *reforestation*, and genetic improvement activities. Provincial ownership of material applies regardless of *deployment* method (natural regeneration, planting, seeding, etc.).

Once authorized by the province through licenses, permits or otherwise, an organization or person(s) owns the trees that have been harvested or other physical material that is collected from *public land* for the purpose of tree improvement. This ownership right remains until the material is deployed back on to *public land*, at which time the right transfers to the province.

Some exceptions apply:

- The province reserves the right to retain some collected material for conservation or research purposes. (See Standards 17.0, 29.2, 29.3 and 29.4 for more detail). Such material may be shared with research agencies, but the province will inform those recipients that they cannot distribute material or genotype-specific information on the material. The intent is to encourage use of material for knowledge creation and research, while establishing limits on the distribution of material.
- The province may reserve the right to *genotypes* and intellectual property wholly or in part developed from forest material collected from Alberta *public land* when such material is utilized for commercial means. This is outlined in more detail in the next section of this document, "Management of Intellectual Property."

- Forest Management Agreement (FMA) holders have ownership rights to timber on land subject to an FMA and are entitled to compensation for any damages to timber or improvements they have created (such as genetically improved material that has been deployed on *public land*).

8.0 Management of Intellectual Property

For the purpose of these standards, intellectual property (IP) is considered to be all genetic information that is attributable to specific tree material and associated *genotypes*, and associated rights to take out a patent on such *genotypes*. IP resulting from forest genetics and tree improvement research and development projects will be shared between the province, forest company, research organization and/or tree improvement cooperative in accordance with the following principles.

a) The province recognizes that ownership of IP rights should be based on the degree of effort by parties involved in a breeding or research program in which the province is a cooperator. Effort is generally considered to be financial investment, but may include in-kind contributions such as, but not limited to, facility use, provision of material and scientific support for a specific breeding program. The greater the level of effort, the greater should be the rights to IP. Respective rights to intellectual property should be defined in an agreement between the province and other members of the cooperative.

b) The province will endeavor to retain benefits in the form of revenue whenever material from *public land* is utilized for commercial means. However, the province will not seek to obtain revenue when material is used for the *deployment* or strengthening of tree improvement programs in Alberta. Exchanges of material between Alberta and other jurisdictions will generally not be considered for royalties, as such exchanges benefit the province and provincial tree improvement.

Implementation

For existing and future tree improvement cooperatives involving the province, the province will endeavor to establish agreements that define the respective intellectual property rights of all parties.

For collections of material by parties who do not hold timber dispositions and associated *reforestation* obligations in Alberta, a Temporary Field Authority (TFA) and collection plan is required as per Standards 11.1.3 and 11.1.4. A condition may be placed on such TFA authorizations stating that the province will retain all intellectual property rights to material collected, unless otherwise defined in an agreement.

The province will endeavor to define commercialization arrangements by way of an agreement at the earliest opportunity, wherever possible. The province may also directly charge a collection fee or royalty on material collected from *public land* when material is for commercial ventures (i.e. sale of genetically improved material and associated information) that are unrelated to tree improvement or are outside Alberta.

Rights Authorizations

The owner of material and intellectual property may authorize another to exercise the owner's rights by way of agreement. The types of rights that might be addressed are *material use rights*, *breeding rights* or commercial sales rights. For example, other provinces in Canada have utilized an agreement called a *material transfer agreement* to specify such rights.

Such agreements may be required between the Department and any other entity – industrial, academic or research – involved in tree improvement activities in Alberta, nationally or internationally. Some situations where these agreements may apply are:

- where a third party wishes to use materials and associated *genotypes* from a tree improvement program involving the Department or *public land* for propagation or further breeding for commercial or profit objectives, and
- where any member of a cooperative involving the Department wishes to use material and associated *genotypes* for propagation or further breeding outside the cooperative(s) where they are participants.

9.0 Access to Data and Information

The Department will have access to data and information pertaining to improved stock and/or research and breeding programs. This access is required because of the Department's stewardship responsibility to monitor for diversity and adaptation of materials to be deployed on forested *public land*. Specific data needs will be outlined in plan submission and reporting requirements as determined in other sections of this document.

All information provided to government, or in the custody or control of government, can be potentially disclosed under FOIP (Freedom of Information and Protection of Privacy) legislation if a request for disclosure were made. It is recognized that cooperative tree improvement programs with government and any other party's information submissions to government are subject to FOIP legislation, and that other parties may request access to information through FOIP requests. The Department will refuse to release information from cooperative programs that meet all conditions as per section 16 of the FOIP Act.

In summary, disclosure would be refused where information:

a) would reveal trade secrets or scientific/ technical information of a third party, and
b) would harm the competitive position of a third party or result in undue financial loss or gain to any person or organization, and
c) is supplied in confidence to the Department.

MATERIAL COLLECTION, HANDLING, REGISTRATION AND STORAGE (MCHRS)

Goals

Genetic materials of forest trees intended for operational *deployment* on *public land* will be collected, handled, registered and stored in a way that is designed to:

- ensure adaptation and diversity,
- maintain documented *genetic identity* and ensure materials are appropriately tracked, and
- ensure that the genetic integrity and physical quality of materials are maintained.

MCHRS Standards

10.0 Registration

10.1 All material to be *deployed* on *public land* must be registered with the Department. See Appendix 2 (*Stream 1*) and Appendix 3 (*Stream 2*) for applicable forms.

10.2 Requests for *registration* are subject to review and acceptance by the Department. If one or more of the following standards are not met, material may not be registered.

10.3 Required *registration* information must be complete, accompanied by the signature of the owner or registrant and submitted to the Department (Provincial Seed Officer). All collection, handling, storage and processing information is to be made available for Departmental review upon request.

10.4 Material that does not meet requirements for *unrestricted registration* may be eligible for *restricted registration* or for holding, pending *registration* eligibility (e.g. insufficient number of parents). See Appendices 2, 3, 4, and 5 for registration requirements.

10.5 Upon *registration*, the Department will assign the *registered lot number*.

Stream 1 material

10.6 For *registration* of *Stream 1 material* the material collection criteria defined in Appendix 4 must be met.

10.7 For *registration* of *Stream 1 material* the following basic information is required and is to be recorded on the registration form (Appendix 2): owner, species, type of material, source location, horizontal extent of collection, the elevations of the highest and lowest collection point, *seed zone*, collection dates, number of parents, ARIS code (Appendix 6), amount being registered, storage location and signature of registrant.

10.7.1 For *registration* of *Stream 1* **seed**, the following additional information is required: *temporary lot number*, volume of cones collected (conifer), yield, viability or germination %, purity, moisture content and 1000 seed weight.

10.7.2 For *registration* of *Stream 1* **vegetative material**, no additional information is required.

10.8 Material meeting *unrestricted registration* requirements (see Appendix 4) is eligible for *deployment* up to 1 km outside the *seed zone* of origin (see Appendix 7) provided the difference in elevation between point of collection and point of deployment does not exceed 100 m. Such material is also eligible for transfer across a seed zone boundary according to the processing Standard 18.2.5.

Stream 2 material

10.9 For *registration* of *Stream 2 material* (see Appendix 3), the *effective population size* criteria contained in Appendix 5 must be met.

10.10 *Stream 2* material must originate from a Department-*approved facility* (see Standards 32.2 and 32.7).

10.11 For *registration* of *Stream 2 material*, the following is required: *temporary lot number*, owner, species, type of material, *production facility*, collection dates, amount being registered, storage location, list of parents represented, *crop genetic worth* (where available), *deployment zone*, *effective population size*, ARIS code (Appendix 6) and signature of registrant.

10.11.1 For *registration* of *Stream 2* **seed**, the following additional information is required: volume of cones collected (conifer), yield, viability or germination %, purity, moisture content and 1000 seed weight.

10.11.2 For *registration* of *Stream 2* **vegetative material,** the contribution (%) of each clone to the vegetative lot is required.

Restricted registration

10.12 *Restricted registration* (see Appendices 2 and 3) may apply where:

- documentation standards of 10.7 above have not been met, OR
- collections (*Stream 1*) do not meet requirements for *unrestricted registration* (see Appendix 4), OR
- documentation standards of 10.11 above have not been met, OR
- *effective population size* (*Stream 2*) is less than that required for unrestricted registration (see Appendix 5), OR
- *Stream 2 material* is derived from non-local sources (e.g. non-local provenances, non-local species, non-local hybrids, *genetically modified organisms* as determined on a case-by-case basis).

10.13 Conditions on deployment may be applied on *restricted registration* material. See Standard 18.2.6 and Appendix 8 (*Stream 1*); Standard 18.4 and Appendix 9 (*Stream 2*).

11.0 Collection

11.1 Collections from public land

11.1.1 All collections of seed and vegetative material intended for *reforestation* or for research supporting reforestation that is carried out on *public land* require an authorization from the Department as per Timber Management Regulation 141.5.

11.1.2 Proponents responsible for *reforestation* will outline their intent to collect in their Annual Silviculture Schedule. The Department is to be notified of the target species and location of a collection 48 hours prior to a collection taking place.

11.1.3 Collections of forest tree material other than those identified in 11.1.2 above require a temporary field authorization (TFA) from the Department field office (Appendix 10). The proponent(s) will submit a map and collection plan identifying the area of collection, type of material, method of harvest, timing and target species.

11.1.4 Authorization for native plant material collections not intended for *reforestation* requires a TFA and must follow the *Native Plant Revegetation Guidelines for Alberta* (see the Alberta Agriculture website).

11.1.5 For collections falling within legislated protected areas, permits will be required from Parks and Protected Areas, Alberta Community Development.

11.1.6 Genetic material collected from *public land* for research or *controlled parentage programs* (CPP) will be documented on the appropriate form (Appendix 11 or 12) and submitted to the Department (in either hard copy or electronic format) within six months of collection completion.

11.2 Each disposition holder will maintain a minimum of one registered Stream 1 lot for each species, in each seed zone where artificial regeneration is planned. In the event that no seed is available, refer to Appendix 8 and Appendix 13.

11.3 The maximum registered seedlot or vegetative lot size will depend on numerical restrictions on deployment from a single seedlot or vegetative lot. Maximum numbers deployable by seed zone size are as shown in Appendix 14.

11.4 Stream 1 vegetative material may be multiplied in stoolbeds established from collections that contain the required minimum number of trees per collection for Stream 1 material (see Appendix 4 – Material Category D).

11.5 Genetic material collected from sources other than public land (non-local) will be documented on the appropriate form (Appendix 15) and submitted (in either hard copy or electronic format) to the Department upon entry into an approved controlled parentage program or prior to deployment in research tests on public land.

11.6 Collections from approved production facilities

11.6.1 Collections from Department-approved *production facilities* do not require an authorization (see PCPM Standards for collection standards and guidelines).

12.0 Transportation of Material

12.1 A proper identification tag must accompany each container of material/cones from the time of collection to delivery to the processing and/or storage facility.

- Identification for *Stream 1 material* must include the *temporary lot number;* the material's owner; Section, Township, Range and Meridian; year of collection and species.
- Identification for *Stream 2 material* must include the *temporary lot number*, the material's owner, orchard number, year of collection and species.

12.2 When research or CPP parent material is collected, shipped or stored, it must be accompanied by the Transportation and Storage Label Form (Appendix 16) and either the *accession number*, *registered lot number* or *unique identifier*.

12.3 Transportation of materials from public land

12.3.1 A completed Registration Request Form - Stream 1 (Appendix 2) must accompany all shipments of *public land collections* of seed and vegetative material intended for *reforestation*.

12.4 Transportation of materials from an approved production facility

12.4.1 A completed Registration Request Form - Stream 2 (Appendix 3) must accompany all cone and material shipments.

12.5 Withdrawal and transportation

12.5.1 A completed Reforestation Seed and Vegetative Materials Withdrawal and Transportation Form (Appendix 17) must be received by the Department (Provincial Seed Officer) before a seed or vegetative material withdrawal may be made.

12.5.2 Unless approved by the Department (Provincial Seed Officer), withdrawals of seed or vegetative material for *deployment* are not permitted until *registration* is complete.

12.5.3 A Reforestation Seed and Vegetative Materials Withdrawal and Transportation Form (Appendix 17) is to be used for tracking materials from withdrawal from storage through to nurseries or related facilities. The Department (Provincial Seed Officer) is to be notified of any deviation from the original documentation.

13.0 Processing

13.1 Processing of seed for operational deployment must be carried out at a seed processing facility approved by the Department. In order to be approved, seed processing facilities must have the verifiable capability to maintain accurate identity and seedlot integrity. For a list of approved seed processing facilities, see the Department's website.

13.2 Seeds and vegetative materials must have verifiable identity documentation, and the integrity of individual lots must have been maintained throughout the process. Any mixing of collections must be done and documented in such a way that the eventual distribution of individuals can be assured to be random within the deployment lot.

13.3 Seed shall be processed and delivered for storage within six months of collection.

13.4 The completed Registration Request Form (Appendix 2 or Appendix 3) must accompany the seed to the Alberta Tree Improvement and Seed Centre (ATISC) or other recognized storage facility for registration.

13.5 Where seed and vegetative material lots are split for any reason, the Registration Request Form (Appendix 2 or Appendix 3) must be included with each portion.

13.6 Seed processing facilities are not permitted to withhold any reforestation seed or ship reforestation seed to any location except ATISC or another approved storage facility without the written permission from the seed owner and the Department (Provincial Seed Officer).

14.0 Seed Testing

14.1 Seed testing must be conducted in accordance with the Department's Seed Testing Guidelines, which are published on the Department's website or supplied by ATISC.

14.2 An experienced seed testing technician or laboratory scientist responsible for the seed testing laboratory must sign seed test result reports.

15.0 Storage

15.1 All registered seed must be stored at ATISC or another storage facility approved by the Department.

15.2 Registered vegetative materials that need to be maintained in growing conditions for propagule production must be stored or maintained at an approved storage facility. An approved *production facility* undertaking propagule production for *deployment* on *public land* is considered an approved storage facility.

15.3 The Department will review requests for approval of storage facilities other than ATISC on the basis of physical infrastructure and management processes.

15.4 Seed and vegetative material received for storage must be securely packaged and labeled with the temporary or *registered lot number* as written on the accompanying Registration Request Form - Stream 1 (Appendix 2). Containers must have one tag inside and one tag securely affixed to the outside.

15.5 All seed and vegetative materials storage facilities must follow handling and storage procedures that maintain lot identity and integrity.

15.6 For storage of unregistered collections not originating on *public land*, or of seed and vegetative materials obtained from other agencies, the minimum information required is: species, seed source, moisture content, 1000 seed weight and total seed amount submitted for storage at ATISC or other approved storage facility.

16.0 Excess Seed, Seedlings and Vegetative Material

16.1 Nurseries and/or propagation facilities are not permitted to sell or distribute excess seed, seedlings or vegetative material for *deployment* on *public land* without prior approval of the material owner and the Department (Provincial Seed Officer). Exchanges of material between material owners does not require Department approval as long as the standards within this manual are followed with deployment of the material.

17.0 Retention of Material for *Ex Situ* Conservation

17.1 The Department has the right to retain samples of tree seed and vegetative material collected from *public land* for the purpose of conservation of *wild* seed or vegetative genetic resources.

17.1.1 For *Stream 1* seedlots, the Department may, at the time of *registration*, access up to 30,000 viable seeds or 5% of the initial total seedlot, whichever is less. The Department will notify the owner of any withdrawals. Amounts greater than this will require written consent of the company.

17.1.2 The Department may access *Stream 2 material* with written consent from the company.

17.1.3 For seed collections from *public land* intended for inclusion in research or *controlled parentage programs* in Alberta, the Department may request that 5% of the seed be provided to the Department.

17.1.4 For all other *public land* seed or vegetative material collections not intended for *reforestation* or tree improvement in Alberta, the Department may request that 10 % of harvested seed or vegetative material be provided to the Department.

GREEN AREA DEPLOYMENT (GAD)

Goals

Genetic resources of forest trees will be deployed within the *Green Area* in a way that strives to:

- conserve the genetic integrity, adaptability, diversity and health of *wild* and managed populations while recognizing that genetic change will occur through evolutionary pressure, breeding and *deployment*,
- maintain or enhance forest productivity,
- be consistent with sustainable forest management principles (economic, social and environmental sustainability), and
- recognize that the Detailed Forest Management Plan (DFMP) or plans of an equivalent level, guided by this and other related policies, will determine how *deployment* will occur.

GAD Standards

18.0 Deployment of Registered Material

18.1 General

18.1.1 Only registered materials – unrestricted or restricted – may be deployed within the *Green Area* (see exceptions in Standard 19.0).

18.2 Deployment of Stream 1 materials

18.2.1 *Stream 1 materials* are collected for *deployment* within the *seed zone* of origin. *Seed zones* are those delineated on the Seed Zone Map provided in Appendix 7.

18.2.2 For seed and vegetative material collections made before May 1, 2003, the need for a variance approval to move seed outside the *seed zone* of origin will be determined from the decision tree in Appendix 13.

18.2.3 To maintain population diversity within a *seed zone*, total seedling and/or vegetative material *deployment* from *Stream 1* sources with *unrestricted registration* will be limited on the basis of *seed zone* size as set out in Appendix 14.

18.2.4 Unrestricted material collected as set out in Appendix 4 is eligible for application for *deployment* outside the *seed zone* of origin (see Appendices 8 and 13 for procedures). Unrestricted material may, without applying for a variance, be deployed within 1 km of the *seed zone* boundary, provided elevation from the point of collection (mid-point of range) to the point of *deployment* does not exceed 100 m. See Appendix 14 for additional *deployment* considerations.

18.2.5 Movement of seed or vegetative propagules outside the *seed zone* of origin requires variance approval.

- Variances for *Stream 1 material* may be requested by submitting a Request for Deployment Variance for Stream 1 Material (Appendix 8) to the Department (Provincial Seed Officer).
- Where the same variance to deploy seed outside the *seed zone* of origin may be requested several times, a standing approval may be issued for a five-year period.
- Any three requests for the same variance, or any standing approval, will trigger a request for the Department (Provincial Seed Officer) to review the *seed zone* boundaries and seed or vegetative material collection practices.

18.2.6 For *deployment* of restricted *Stream 1 material*, a determination is to be made by the Department on the basis of a request for variance (Appendix 8).

18.3 Seed zone development and amendment

18.3.1 Requests for review and amendment of *seed zone* boundaries will be reviewed by the Director of the Forest Management Branch. Reviews will be based on ecological and genetic information.

18.3.2 Development of *species-specific seed zone*s will require *testing* according to Standard 28.4.

18.4 Deployment of Stream 2 materials

18.4.1 *Deployment* of *Stream 2 material* as clonal blocks or rows is addressed through assessment as per Standard 19.0 or through assessment as per Appendices 1 and 9.

18.4.2 Total seedling and/or vegetative material *deployment* from *Stream 2* sources from a given *production facility* or facilities will be limited by *breeding region* or *deployment zone* as defined in the Controlled Parentage Program (CPP) Plan (see Appendix 18). For a list of existing *breeding regions*, see Appendix 19.

18.4.3 Total *deployment* of *Stream 2* seed for a given *deployment zone* will be limited by the *cumulative effective population size (Ne)* of the output from associated orchard(s). The total *deployment* from the associated orchard or orchards, where estimated *cumulative Ne* summed over the life of the orchard(s) is less than 30, may not exceed 25% of the total area estimated for the target strata over a rotation. An orchard or orchards with estimated *cumulative Ne* of 30 or more may produce material for *deployment* on up to 50% of the total area estimated for target strata over a rotation. *Deployment* numbers by proponent are presented in the Detailed Forest Management Plan or Annual Operating Plans and identified in the current CPP Plan. Appendix 20 provides details of methods for calculating *cumulative Ne*. Appendix 21 provides the method for calculating *deployment* limits, and an example of the information and format for *production facility* planning and reporting under a CPP Plan.

18.4.4 Total *deployment* of *Stream 2* vegetative materials for a given *deployment zone* will be limited by the *cumulative effective population size* of the output from the associated *production facility* or facilities. The total *deployment* from a *production facility* or facilities, where estimated *cumulative Ne* (summed over the life of the facility or facilities) is less than 30, may not exceed 20% of the total area estimated for target strata over a rotation. A facility or facilities with estimated *cumulative Ne* of 30 or more may produce material for *deployment* on up to 40% of the total area estimated for the target strata over a rotation. *Deployment* numbers by proponent are presented in the Detailed Forest Management Plan or Annual Operating Plans and identified in the current CPP Plan. Appendix 20 provides details of methods for calculating *cumulative Ne*. Appendix 21 provides the method for calculating *deployment* limits, and an example of the information and format for *production facility* planning and reporting under a CPP Plan.

18.4.5 Existing *breeding region* and *deployment zone* boundaries may be periodically reviewed and revised (see Standard 28.0).

18.4.6 Minor changes to existing *breeding region* boundaries may be made with the mutual consent of the proponent(s) and the Department.

18.4.7 Prior to *deployment* of **restricted** *Stream 2 material*, the Detailed Forest Management Plan (DFMP) is to contain a summary of the research *tests* and analysis undertaken, monitoring required, and methods of ameliorating the risks identified in Appendix 9.

18.4.8 A request for movement of seed or vegetative propagules outside the *breeding region/deployment zone* of origin will only be considered in emergencies, and is initiated by submitting a Request for Deployment Variance for Stream 2 Material (Appendix 22) to the Department (Provincial Seed Officer).

19.0 Deployment of Unregistered Material

19.1 *Wild* transplants and cuttings from within 5 km and 100 m elevation of the target planting site may be deployed without *registration*. These transplants and cuttings may not be multiplied or *serially propagated.*

19.2 For a single clone, a maximum of 5000 propagules may be deployed within the *seed zone* of collection.

20.0 *In Situ* Gene Conservation

20.1 *In situ* conservation for *Stream 1 material* or other species not identified in *controlled parentage programs* for a specific *seed zone* will be accommodated through a provincial gene conservation plan as developed.

20.2 Between two and four areas (as per Standards 20.3 – 20.6) of *wild* forest populations (as represented by species and strata class, e.g. timber productivity rating, timber type) are required to be designated for gene conservation for each tree species included in a CPP Plan, in each *seed zone*. A single area may provide conservation for more than one species. The number of gene conservation areas required will depend on *seed zone* size as follows:

Seed Zone Size	Number of Conservation Areas Required
> 1.0 million ha	4 per species
0.5 – 1.0 million ha	3 per species
< 0.5 million ha	2 per species

For sizes of specific *seed zones*, see Appendix 7.

These gene conservation areas may be chosen from:

20.3 existing reserves, OR

20.4 subjective landbase deletions (e.g. streamside buffers, non-merchantable, inoperable), OR

20.5 harvestable areas dedicated for natural regeneration (e.g. natural seeding, partial cutting, plant with seed specifically from the site, or *wild Stream 1* collections from adjoining areas), OR

20.6 understory protection and variable retention areas (retain some naturals, supplement with planting with seed specifically from the core area [see Appendix 4] or if not available, *wild Stream 1* collections from adjoining areas).

20.7 *In situ* gene conservation areas will be implemented as follows:

20.7.1 Areas designated for gene conservation will be dispersed across the *seed zone* to minimize risk of loss.

20.7.2 Areas designated for gene conservation will be chosen with consideration for long-term protection from biological and non-biological threats. A CNT (Consultative Notation) is recommended for these areas.

20.7.3 Areas will be large enough to meet a reasonable expectation of 5000 trees (at rotation) in a core area with an additional buffer of 500 m around it.

20.7.4 The target species as identified in the CPP Plan will be managed as per the options specified in Standards 20.2 and 21.1.3.

20.8 For a given species, in any *seed zone* where *Stream 2 material* is being planted, the CPP plan(s) will indicate how *in situ* standards are being met. Because *breeding regions/deployment zones* may include more than one *seed zone* and more than one cooperator, cooperative planning among parties in each *breeding region/deployment zone* may be required.

21.0 Deployment Planning and Reporting

21.1 Planning for Stream 2 Deployment

21.1.1 Annual *deployment* schedules, as shown in the Annual Silviculture Schedule of an Annual Operating Plan (AOP), will be consistent with the approved DFMP *deployment* strategies.

21.1.2 In the absence of approved DFMP *deployment* strategies, annual *deployment* schedules will be approved when consistent with production objectives as defined in the approved CPP Plan (see Standard 24.0).

21.1.3 Areas designated for gene conservation will be described in the DFMP, which will also include a statement of intended management on a time horizon of two rotations.

21.2 Reporting

21.2.1 Compliance monitoring of *deployment* activities (*Streams 1 and 2*) will be reported in the Five Year Stewardship Report of the Detailed Forest Management Plan. Performance measures will be DFMP-specific and designed to assure plan assumptions are adequately monitored. At a minimum, cumulative *deployment* of each source/type of material will be reported.

21.2.2 Deployment of all registered material will be reported annually to the Department in the Alberta Regeneration Information System (ARIS).

21.2.3 A map showing *deployment* by cutblock for the past five years' activities, of appropriate scale, will be submitted, when:

21.2.3.1. *restricted registration Stream 2 material* lots are planted, OR

21.2.3.2. *unrestricted registration Stream 2 material* from a given *production facility* exceeds an average of 50% of areas reforested by strata and species in a five-year period.

This will be reported in conjunction with the Five Year Stewardship Report of the DFMP. Digital files will be accepted in lieu of hard copy format.

21.2.4 Compliance with *in situ* gene conservation standards will be indicated by specifying, in the Five Year Stewardship Report, the status of designated areas.

22.0 Post-Deployment Monitoring

22.1 Growth and yield monitoring will be as per the DFMP and FMA requirements.

22.2 Monitoring requirements for *restricted registration* material will be determined through the Assessment of Risk for Stream 2 Material (Appendix 9). This is a case-by-case assessment.

23.0 Genetic Research Plantings

23.1 Research plantings can be established covering an area of up to 17 ha per site. Variances for contiguous research plantings larger than 17 ha may be requested by submitting a Request for Planting Variance for Research Material (Appendix 23) to the Department (Provincial Seed Officer).

23.2 All materials included in research plantings must have a material identity (*unique identifier*, *accession number* or *registered lot number*).

23.3 All research plantings must meet BTV Standards.

23.4 Research plantings that include material of uncertain or unknown adaptation (non-local) require approval through a Research Program Plan or Controlled Parentage Program (CPP) Plan.

23.5 Research plantings including *genetically modified organisms (GMOs)* must comply with both federal regulations and provincial policy.

23.6 A standing approval can be requested for planting material from subsequent collections from the same source.

23.7 Where a previously untested, non-local species or provenance (including hybrids) is to be planted in a research *test* that exceeds 17 ha, a benefit/risk assessment as per Appendix 23 will be required with the variance request.

23.8 Out-of-zone/*breeding region* material may require additional monitoring.

BREEDING, TESTING AND VERIFICATION (BTV)

Goals

Forest genetics programs that produce *Stream 2 material* or information relating to *Stream 2 material* for *deployment* on *public land* in the *Green Area* shall:

- use testing, analysis and documentation protocols that are effective, efficient and scientifically sound, and
- be designed to ensure long-term flexibility in direction and development of *controlled parentage programs*, and
- produce reliable estimates of *genetic gain* when gain is included as an objective of the Controlled Parentage Program (CPP) Plan.

BTV Standards

24.0 Controlled Parentage Programs (CPPs)

24.1 Proponent(s) of CPPs that existed prior to the effective date of these standards and are intended to produce material for *deployment* on *public land* will submit a CPP Plan in electronic or hard copy (see Appendix 18). The date for submission will be determined by consultation between the proponent(s) and the Department.

24.2 New CPPs require an approved CPP Plan. Proponent(s) of new CPPs that are intended to produce material for *deployment* on *public land* will submit a CPP Plan in electronic or hard copy (see Appendix 18). The CPP Plan approval process is initiated when the proponent sends a letter of intent to the Department. The Department will respond within three months of receiving the letter of intent. Provided the proponent submits its plan within 18 months of the letter of intent, resolution can be expected within 24 months after the letter of intent is received.

24.3 Where a new or revised CPP Plan is not approved by the Department, the proponent(s) may request that the Director, Forest Management Branch, appoint a third party to review the technical merit of the plan. The Department will consider the third party's advice and provide a decision.

24.4 CPP plans intended to produce *Stream 2 material* will identify:

- the total area (ha) by participating tenure holder within the target *breeding region/deployment zone*,
- the total operable area (ha) by tenure holder within the *breeding region/deployment zone*,
- the target strata (species by *breeding region*, not yield strata) for which the *Stream 2 production facility* is designed,
- the total area (ha) of target strata by tenure holder,
- estimated plants required for 100% planting of target strata area per rotation for each participating tenure holder,
- estimated annual number of seedlings and/or vegetative propagules from a *production facility* allocated to each participating tenure holder, and
- planned total production of seedlings and/or vegetative propagules over the life of the facility.

24.4.1 To determine *deployment* limits for a *production facility* or facilities and for an example of information and presentation format for CPP planning, refer to Appendix 21 and Standards 18.4.1 through 18.4.4.

- For *Stream 2 restricted registration* material, see also Standards 18.4.7 and Appendix 9.

24.5 **Revisions to Controlled Parentage Program Plans**

24.5.1 When significant changes occur, revised CPP Plans will be submitted to the Department for review. The Department will respond within three months of submission.

25.0 Research Programs

25.1 All genetic testing intended to provide information relating to *deployment* on *public land*, and not currently covered in a CPP Plan, will require a Research Program (RP) Plan to be submitted for approval by the Department (see Appendix 1 and Appendix 24).

25.2 All genetic research field *tests* on *public land* will comply with GAD Standards and field *test* standards where appropriate.

25.3 Upon a request to deploy *non-local material* (or with prior federal approval, *PNTs or GMOs*) on *Green Area public land*, the Department:

- will review all relevant scientific information on a case-by-case basis to evaluate the risks and benefits of *deployment*, and
- may request an RP Plan and additional testing prior to considering inclusion of such material in a CPP.

25.4 Genetic research *test*s intended to produce information relating to *deployment* on *public land* in the *Green Area* will follow applicable standards in Standards 23.0 and 30.0.

25.5 All unregistered material destined for testing on *public land* or for inclusion in *breeding/base population* to be deployed on *public land* will be labelled using *unique identifiers*. (See Appendix 25 for codes and Appendices 11, 12, or 15 for the appropriate submission form.)

25.6 Consultation with the Department is advised if a proponent is intending to establish a realized gain *trial*. The Department can provide clarification regarding an acceptable design and methodology to provide information on strata level *genetic gain*.

25.7 Where a new or revised RP Plan is not approved by the Department, the proponent(s) may request in writing that the Director of the Forest Management Branch appoint a third party to review the technical merit of the plan. The Department will consider the third party's advice and provide a decision.

26.0 Genotype Information and Pedigree Records

26.1 Agencies and companies involved in controlled parentage and research programs with the intent of developing genetic material for *deployment* on *public land* will maintain and submit to the Department:

- complete records of parentage and/or *pedigree* for *genotypes* collected from *public land* (see),
- parentage and/or *pedigree* for *genotypes* established in *production facilities* (see Appendix 15 and Standards 33.5 and 34.4), and
- associated *genotype* information related to species, origin, traits identified in program plans and issues of adaptation or claims for gain (as per genetic *test* analysis reports or requirements arising out of CPP and RP Plans).

27.0 Field Test Data Handling, Storage and Access

27.1 For genetic *test*s established as part of a CPP or RP Plan, an electronic listing will be prepared, in ASCII or another previously agreed-upon format that will allow the unambiguous identification of each *test* tree in the field when accompanied by the appropriate map(s). This listing will contain:

- Department-assigned project number and site identifier (e.g. G625C),
- *test* site name,
- replication/block,
- experimental tree position/location, and
- genetic identity (accession number, registered lot number or unique identifier).

27.2 This file will be submitted to the Department as part of the Genetic Test Establishment Report (see Standard 30.12.1 and Appendix 26).

27.3 Each successive measurement of a genetic *test* is to use the same listing to allow compiling of time series data sets.

27.4 *Validated raw data* will be submitted to the Department as electronic files using the listing defined in Standard 27.1 to identify individual trees.

27.5 *Validated raw data* will be accompanied by a data dictionary describing measurement methods and procedures, variables, format, measurement units and measurement codes, quality control procedures and results, assessors, assessment dates and any field assessment comments. Submission of data must follow the reporting standards outlined in Standard 30.0 and Appendix 27.

27.6 Any data or tree code discrepancies identified by the Department in *validated raw data* sets will be reviewed and corrected by the measuring agency (i.e. company, contractor, scientific cooperator).

27.7 For each genetic research *test*, *validated raw data* files will be compiled by the Department as new data are submitted and archived in a secure system with backup.

27.8 The Department requires submission of any edited data sets used to support claims of adaptation, diversity or performance of *test*s established under CPP or RP Plans.

27.9 The Department will provide cooperators with validated raw *test* data in ASCII format, along with required supporting documentation, contingent on the cooperator's right to such material and knowledge.

28.0 Delineation and Revision of Breeding Regions, Deployment Zones and Species-Specific Seed Zones

28.1 Processes used to delineate new *breeding regions or deployment zones* (e.g. provenance/progeny *tests*) will be included in the associated CPP Plan or supporting RP Plan.

28.2 Revision of existing *deployment zones* (including *breeding regions*) may be conducted under an RP Plan or revision to an existing CPP Plan.

28.3 A request submitted to the Department for the establishment of a new *deployment zone (breeding region)* or the revision of an existing *deployment zone (breeding region)* must include all supporting documentation. The Department will respond within three months of submission.

28.4 Establishment of *species-specific seed zone*s will require an RP Plan and genetic provenance testing for adaptation.

29.0 *Ex Situ* Conservation of Native Species

29.1 General

The Department will be notified of plans to terminate any genetic *test*, clone bank or orchard of native Alberta material on public or private land prior to termination of genetic material. Documentation on genetic material identity will be made available to the Department.

29.2 Samples of genetic tests – public land

29.2.1 When genetic *test*s on *public land* have fulfilled their purpose, the Department may choose and maintain a sample of *test*s for gene conservation purposes.

29.3 Samples of genetic tests – private land

29.3.1 When genetic *test*s of native species collected from *public land* are conducted on private land, the Department will have the opportunity to negotiate for maintenance of a sample of *tests* or to collect genetic material before it is destroyed. A *material transfer agreement* may be required or a lease agreement considered.

29.4 Clone banks or orchards

29.4.1 The Department will have the opportunity to obtain vegetative material from each native parent selected from *public land* that is being vegetatively propagated. Reciprocal access is provided, and a *material transfer agreement* may be required.

29.4.2 Prior to clone destruction (e.g. through roguing), each party will provide notification and access to the clonal material.

29.5 Reporting and documentation

29.5.1 Documentation for gene conservation in clone banks and samples of genetic *tests* will include a map for access to the site, a list of included genetic materials and their origins, a map showing tree location/position and the name, e-mail address and phone number of the contact company(ies) and person(s), as well as, where it exists, a copy of the *material transfer agreement*.

30.0 Genetic Research Tests

30.1 Analyses of genetic *tests* conducted under a CPP or RP Plan will be reported as outlined in Appendix 28.

30.2 Number of test sites

30.2.1 For progeny *tests* associated with a CPP Plan, data from no fewer than three *test* sites, or the number specified in the CPP or RP Plan, will be used for analyses.

30.2.2 For establishment of new *deployment zone* boundaries for *non-local material*, data from a minimum of five provenance *test* sites will be used. The number of *test* sites may vary depending on the size of the proposed *deployment zone* and will be specified in the CPP or RP Plan.

30.2.3 For revision of *breeding*, *deployment* or *seed zone* boundaries, the number of *test* sites will be specified in the CPP or RP Plan.

30.2.4 For establishment of *species-specific seed zones*, the number of *test* sites will be specified in the RP Plan.

30.3 Site selection and documentation

30.3.1 Sites will be well distributed geographically and elevationally across, and representative of, the actual or proposed *breeding*, *deployment* or *seed zone*.

30.3.2 For acceptance and approval of a *trial* series, a Genetic Test Site Information Form (Appendix 29) must be submitted for each *test* site and approved by the Department.

30.4 Site protection

30.4.1 A protective notation/reservation or appropriate *public land* disposition will be obtained prior to *test* establishment (ISP or MLL).

30.5 Field marking

30.5.1 Field marking will be established and maintained that allows for identification of each *test* tree, complete with an establishment report map(s) and description of all coding systems used. See Appendix 30, "Example of Data Collection Map and Corresponding Form."

30.5.2 The starting point for assessments will be clearly and permanently marked in the field and on establishment report map(s).

30.5.3 At least 5% of *test* trees, or the number or proportion specified in the CPP or RP Plan, will have a permanent marker stake.

30.6 Site maintenance – competition and ingress control

30.6.1 Competing vegetation and ingress of the target species will be managed in a manner specified in the CPP or RP Plan to allow free growth and identification of *test* trees.

30.6.2 Ingress of target species, if present or anticipated, will be monitored annually for the first three years and as needed thereafter.

30.7 Site maintenance – maintenance of tree identification

30.7.1 Field labelling will be checked in the year following establishment and at the time of each scheduled measurement. Missing or illegible labels will be replaced within four months of each labelling check.

30.8 Monitoring – data submission

30.8.1 Quality control procedures associated with *test* assessments will be detailed in the Genetic Test Measurement Report (see Appendix 27).

30.9 Monitoring – timing

30.9.1 Growth traits on a given field *test* site will be measured within one dormant season.

30.10 Monitoring – variables

30.10.1 Survival code and other variables specified in the CPP or RP Plan will be recorded at each measurement.

30.10.2 The height of trees shorter than 3 m will be measured to the nearest cm. Trees of height greater than 3 m will be accurate to the nearest dm (i.e. 0.1 m). Units of measurement must be consistent for traits in the measurement period (e.g. all heights in cm).

30.10.3 Height will be measured to within 2% of true values 95% of the time, based on the use of standard measurement equipment, measurement procedures and sampling precision.

30.10.4 Diameter at Breast Height (DBH) will be measured to the nearest mm and recorded in cm.

30.10.5 The DBH of trees larger than 10 cm will be measured to within 5% of the true value 95% of the time. Smaller trees will be measured to within 5 mm 95% of the time.

30.11 Monitoring – duration of measurements and long-term monitoring

30.11.1 Duration of measurements will be specified in the CPP or RP Plan.

30.11.2 Long-term monitoring will be specified in the CPP or RP Plan.

30.12 Monitoring – reporting

30.12.1 A Genetic Test Establishment Report (see Appendix 26) will be submitted to the Department by April 30 of the year following establishment.

30.12.2 A Genetic Test Measurement Report (see Appendix 27) will be completed and submitted together with *validated raw data* sets in electronic format within eight months of completion of the current year's measurements. Data sets will be cleaned and formatted.

30.13 Termination of genetic test, clone bank or orchard

30.13.1 See "Ex Situ Conservation," Standard 29.0.

31.0 Genetic Gain Approval

31.1 The process for approval of *genetic gain* begins with a request by a proponent to the Department, stating an average value expected for specific traits. The Department will provide a response to a request within three months of receipt.

31.2 Approval of a *genetic gain* value will be based on review of the CPP Plan and one or more of:

- associated RP Plans,
- results of genetic *tests* (e.g. *genetic worth* calculation – Appendix 31),
- literature review,
- expert opinion,
- results from other programs, and
- other relevant information.

31.3 Any increase to the AAC attributable to *genetic gain* must be approved through the DFMP process.

31.4 Currently, claims for genetic gain are based on height.

31.5 The minimum age of *test* evaluation in support of a claim for *genetic gain* based on progeny testing will be calculated as:

Minimum age in years = 4 + 0.1 x (midpoint of rotation age class)
as shown in Table 1 below.

Table 1. Minimum test evaluation age to support claims for genetic gain

Rotation age	Midpoint of rotation age class	Minimum evaluation age
6-15	10	5
16-25	20	6
26-35	30	7
36-45	40	8
46-55	50	9
56-65	60	10
66-75	70	11
76-85	80	12
86-95	90	13
96-105	100	14
106-115	110	15
116-125	120	16

31.6 For *non-local material*, adaptation and yield may be assessed on the basis of performance at the age of 20 years or half the anticipated rotation age, whichever is earlier.

PRODUCTION OF CONTROLLED PARENTAGE MATERIALS (PCPM)

Goal

Stream 2 seed and vegetative materials of controlled parentage for *deployment* on *public land* will be produced:

- in Department-approved *production facilities* using established procedures,
- in a manner that maintains the potential to produce a *crop* that can be registered with a calculated *effective population size* (diversity) and *crop genetic worth*, and
- in a manner that ensures that documentation and reporting provide verification of claims for *registration* of materials produced.

PCPM Standards

32.0 General

32.1 Operational *production facilities* and procedures must have the potential to produce registered *crops* of seed or vegetative materials for *deployment* on *public land*.

32.2 The Department will approve facilities for production of materials on the basis of a review of an application submitted to the Department, preferably prior to selecting a *production facility* location. An application will include a risk assessment that will address the following where appropriate:

- pollen contamination for proposed orchard,
- infrastructure (e.g. roads, water source, labour supply, expansion capability, facility modification),
- environment,
- potential pest risks,
- security in space and time, and
- preconditioning/adaptation (e.g. for production environments differing significantly from *deployment* environments).

32.3 A *production facility* on *public land* must be protected by a *public land* disposition or other notation.

32.4 Each *production facility* is designated for a single specified *deployment zone* to ensure adaptation.

32.5 Production of controlled parentage materials must be integrated with an approved Controlled Parentage Program (CPP) Plan. Such facilities may have multiple objectives (e.g. clone bank plus production).

32.6 The maximum amount of registered *Stream 2 material*, over the life of a *production facility* or facilities for a given *deployment zone*, will depend on numerical restrictions on total *deployment* from the *production facility* or facilities (see Appendices 20 and 21). The maximum number deployable will vary by *breeding region* or *deployment* zone, and will be included in the CPP Plan as per Standard 24.0.

32.7 A facility review will include inspection of each *production facility* to assess the ability of the owner to fulfil Department requirements.

- Owners of existing facilities will provide the Department with information supporting Department approval.

32.8 Continued compliance with approval conditions is required to maintain an approval to produce material for *public land deployment*. Technical audits may be used to verify compliance.

32.8.1 Completed Production Facility Establishment Reports and addenda (or equivalent) must be submitted by February 28 as outlined in Appendix 32. A sample establishment report is available on the Department's website.

32.8.2 All orchards must follow the Permanent Sample Tree (PST) Protocols contained in Appendix 33.

32.8.3 All orchards must follow the Phenology and Pollen Monitoring Protocols contained in Appendix 34.

32.8.4 An Annual Operations Report shall be submitted by February 28 as outlined in Appendix 35.

32.9 An approval will be reviewed every five years, or sooner where significant changes to the facility have occurred.

32.10 An approval may be cancelled for failure to comply with the standards or for submitting information that is known to be incorrect or purposely misleading.

33.0 Seed Material Production

33.1 An orchard must be designed to produce a seed *crop* of a minimum *effective population size* of 18.

33.2 Orchards must be designed using specialized design software (e.g. SOL32 or SOMAD).

33.3 *Crop genetic worth* is calculated according to the procedures outlined in Appendix 31.

33.4 *Effective population size* is calculated according to procedures outlined in Appendices 36 and 37.

33.4.1 The basis for collecting required data to calculate the *effective population size* is through sampling of contributing parents as outlined in Appendix 37.

33.4.2 Calculations will be documented and records/data retained and provided upon request for possible auditing.

33.4.3 Where a *seed orchard* with *cumulative Ne* of less than 30 has reached its limit for total production (see Standard 18.4.3 and Appendix 21), a replacement orchard will be required. The new orchard, together with the previous orchard, must have a planned *cumulative Ne* of at least 30. Appendix 20 provides details of methods for calculating *cumulative Ne*.

33.4.4 Material deployed from a *rolling front orchard* must have a *cumulative Ne* of at least 30 by the time 50% of the target strata area has been regenerated with that material (see Appendix 21). Appendix 20 provides details of methods for calculating *cumulative Ne*.

33.5 The *genetic identity*, and where available the *pedigree*, of *seed orchard* parents must be maintained.

33.6 Documentation for each *crop* submitted for *registration* must include:

- owner,
- species,
- type of material,
- *production facility*,
- collection dates,
- *temporary lot number*,
- amount being registered,
- storage location,
- *crop genetic worth* (Appendix 31),
- *deployment zone* (Appendix 19),
- *effective population size* (Appendix 36),
- ARIS code (Appendix 6),
- signature of registrant, and
- seedlot composition (proportion of the seedlot contributed by clone/family).

34.0 Vegetative Materials Production

34.1 *Crop genetic worth* is calculated according to procedures in Appendix 31.

34.2 A vegetative lot must be assembled from *production facilities* to produce a *crop* minimum *effective population size* of 18 for *unrestricted registration.*

34.3 *Effective population size* is calculated according to procedures in Appendix 36.

34.3.1 The individual clonal contribution to a *crop* must be known in order to meet data requirements for calculating *effective population size* for *Stream 2* vegetative materials in Appendix 36.

34.3.2 Calculations will be documented and records/data retained and provided upon request for possible auditing.

34.3.3 Where a *production facility* or facilities for vegetative material with *cumulative Ne* of less than 30 has reached its limit for total production (see Standard 18.4.4 and Appendix 21), a replacement facility will be required. The new facility, together with the previous facility, must have a planned *cumulative Ne* of at least 30. Appendix 20 provides details of methods for calculating *cumulative Ne*.

34.4 The *genetic identity*, and where available the *pedigree*, of clones in the *production facility* must be maintained.

34.5 *Documentation* of each *crop* submitted for *registration* must include:

- owner,
- species,
- type of material,
- *production facility*,
- collection dates,
- *temporary lot number*,
- amount being registered,
- storage location,
- *crop genetic worth* (Appendix 31),
- *deployment zone* (Appendix 19),
- *effective population size* (Appendix 36),
- ARIS code (Appendix 6),
- signature of registrant, and
- genetic composition (proportion of the vegetative lot contributed by clone/family).

GLOSSARY OF TERMS

Term	Definition
Accession number	Four-digit number historically assigned by the Department to research seedlots. These may include individual family collections or bulked seedlots. Accession number is one category of *genetic identity*.
Adapted material	Material resulting from natural evolution, or breeding and testing, that is capable of adequate growth and reproduction in a given habitat and that will not have adverse impacts on the health, functioning and productivity of the ecosystem.
Afforestation	The establishment of a tree *crop* on an area from which the crop has always been absent, or absent for a very long time.
Amplified family	An aggregate of multiple vegetative propagules from each of several to many members of a half- or full-sib family.
Approved facility	A designation provided to a facility that is qualified to produce material for *deployment*.
Base population	The population of trees from which individuals are chosen to establish the *breeding population* and/or *production population* for a *controlled parentage program*. Generally refers to a *wild* population within a *breeding region*; may include trees from adjacent or other regions.
Breeding population	A set of trees within which crosses are made to generate material for the next cycle of selection. Breeding populations are generally large, as compared to the *production population*.
Breeding region	A geographic area, defined mainly by adaptation criteria, for which *Stream 2 materials* are selected, bred, tested, multiplied and deployed.
Breeding rights	The right to use genetic materials for one or more generations of crossing, genetic testing and selection. These rights are usually exercised by tree breeders to produce successive generations of improved materials.
Breeding value (BV)	The genetic value of an individual for a given trait, based on the mean performance of its offspring or other relatives. BV may be expressed in terms of measurement units such as m or cm; it is more commonly expressed in relative terms, as a percent deviation from the population mean.
Collections, public land	Genetic material gathered and removed from *public land* for the purposes of *reforestation*, breeding or research. It does not include collections from approved *production facilities*.
Controlled parentage program (CPP)	A stock production program that includes in its population a finite number of deliberately chosen individuals. Production of *deployment* stock for the program occurs in a *production facility* (such as a *seed orchard* or *stoolbed)* where parents are propagated vegetatively or sexually.
Crop	Aggregate of cones, seeds or vegetative propagules intended to be registered under a single *registered lot number*.
Cumulative effective population size	The effective population size (*Ne*) of the output of a *production facility* or facilities, or of material deployed from that facility or facilities, calculated over years and/or across *production facilities*, for a given *breeding region* or *deployment zone*. See Appendix 20 for calculation method.
Cumulative Ne	See "Cumulative effective population size."
Deployment	Establishment of a new *crop* through artificial regeneration; through physical movement from one site (e.g. a nursery) to the *deployment* site; or through planting or seeding designed to meet resource management objectives or obligations. *Afforestation, reclamation* and *reforestation* may be considered to be *deployment*. Natural regeneration, even where enhanced through silvicultural techniques such as scarification, is not considered to be *deployment*.

Term	Definition
Deployment zone	A geographic area, defined mainly by adaptation criteria, for which *Stream 2 material* is produced. Deployment zones include *breeding regions*.
Dioecious	Refers to a species in which male and female "flowers" generally occur on different plants; thus each plant is usually either male or female, but not both; e.g. aspen *(Populus tremuloides)*.
Effective population size (Ne)	Effective population size (Ne) is one measure of genetic diversity and relatedness in a seed or vegetative lot, and reflects both the degree of relatedness among parents and the degree of balance among parental contributions to the given lot.
Effective population size, cumulative	See "Cumulative effective population size."
Genetic gain	The average heritable change attributable to selection in a given trait, from one generation to the next.
Genetic identity	One of several unambiguous current or historical identifiers of seed or vegetative material lots that can be used to identify the genetic source of material in a trial. The *unique identifier*, *accession number* or *registered lot number* may be used.
Genetic research planting	A planting associated with a research plan or *controlled parentage* plan. All materials in genetic research plantings must be *Stream 1 materials, Stream 2 materials, local research materials* or *non-local research materials,* and must be registered or have a material identity.
Genetic worth	For a seed or vegetative lot, the predicted difference in value of a given trait (e.g. height or volume) from the value of that trait in *wild* stand material.
Genetically modified organism (GMO)	An organism that, through human intervention in a laboratory, has had its genome, or genetic code, deliberately altered through the insertion of a specific identified sequence of genetic coding material (generally DNA) that has been either manufactured or physically excised from the genome of another organism. Genetic modification may be used to alter any of a wide range of traits, including insect and disease resistance, herbicide tolerance, tissue composition and growth rate.
Genotype	The *genetic identity* or constitution of an individual. Physical material, in the form of plant tissue, provides the medium for storage and transmission of a genotype.
Green Area	The area outlined and colored green on a map annexed to the Order Classifying Public Lands dated April 16, 1963, and published in *The Alberta Gazette* on April 30, 1963, as amended from time to time. The *Green Area* includes *public land* that is primarily forested, and is managed for timber production, oil/gas development, watershed, wildlife and fisheries, recreation and other uses.
Hybrid orchard	An orchard including non-hybrid parents that is managed to produce hybrid seed. This term does not apply to orchards that include naturally occurring hybrid parents (e.g. Sw x Se).
Intellectual property rights	The rights to intangible property that is the product of the human intellect. Intellectual property may be protected by copyright, trademark or patent. The holder of intellectual property rights is usually the person or persons who developed the product or the organization that funded it. In the context of Forest Genetic Policy, intellectual property rights apply to genetic data and to the *genotypes* to which they apply, either separately or in aggregate.

Term	Definition
Local research material	See "Research material, local."
Locally adapted material	Material from, or derived from, the *seed zone* or *breeding region* in question. Locally adapted material may be one of: 1. *Stream 1 material* collected from within the *seed zone* in which *deployment* is planned 2. *Stream 2 material* collected from a *production facility* associated with a *controlled parentage program* for the *breeding region* within which *deployment* is planned 3. *research material* collected from a *breeding region* (or, in some cases, adjacent *breeding regions*) for inclusion in a *controlled parentage program* for the *deployment zone* within which *deployment* is planned
Lot number, registered	A number used to uniquely identify a seed or vegetative lot through to storage, *deployment* and monitoring. The registered lot number is assigned by the Department when material is registered.
Lot number, temporary	A number used to uniquely identify a seed or vegetative lot prior to *registration.*
Material transfer agreement (MTA)	Material transfer agreements (MTAs) are contractual legal agreements between two or more parties governing the transfer and subsequent use of genetic materials. MTAs specify which rights are conferred, and may contain clauses concerning such topics as record keeping, reclaim rights, liability disclaimers and prohibitions on use of the material for further breeding.
Material use rights	The right to use genetic materials (e.g. seeds, seedlings, somatic seedlings or rooted cuttings) for plantation purposes. The holder of material use rights does not usually have propagation or *breeding rights.*
Monoecious	Refers to a species in which male and female "flower" parts generally occur on the same plant, either within a single "flower" or separately; thus each plant is usually both male and female; e.g. white spruce *(Picea glauca)*.
Ne	See "Effective population size."
Non-local material	Material of unknown adaptation. Any of: 1. *wild* material collected from outside the *seed zone* in which *deployment* is proposed, 2. *controlled parentage program* material collected from a *production facility* not associated with the *deployment zone* within which *deployment* is proposed, or 3. material from outside the given *deployment zone*, under evaluation for adaptation.
Non-local research material	See "Research material, non-local."

Term	Definition
Pedigree	A record of parentage, sometimes also including data on the performance of parents and other relatives.
Plants with Novel Traits	A plant variety/genotype possessing characteristics that demonstrate neither familiarity nor substantial equivalence to those present in a distinct, stable population of a cultivated species of seed in Canada and that have been intentionally selected, created or introduced into a population of that species through a specific genetic change. In this definition, familiarity means, the knowledge of the characteristics of a plant species and experience with the use of that plant species in Canada and substantial equivalence means, the equivalence of a novel trait within a particular plant species, in terms of its specific use and safety to the environment and human health, to those in that same species, that are in use and generally considered as safe in Canada, based on valid scientific rationale.
Production facility	An entity such as a *seed orchard*, *stoolbed*, hedge or laboratory where *Stream* 2 seed or vegetative material is produced for *deployment* through sexual reproduction or vegetative propagation.
Production population	The population of trees that produces seeds or cuttings for stock production for *deployment*. This will generally be a subset of the *base population*, or of the *breeding population* if one exists, and may or may not be intensively selected. The production population is usually much smaller than the *breeding population*.
Public land	Alberta "public lands" as defined in the *Public Lands Act*. Includes *Green Area* (land managed primarily as forest land) and *White Area* (land managed primarily for agriculture and uses other than forestry).
Public land collections	See "Collections, public land."
Ramet	An individual that has been vegetatively reproduced from the original plant, or *ortet*, and is thus genetically identical to it.
Ramet, grafted	A ramet created by grafting a twig or bud from the original plant onto a physically distinct rootstock. The portion of the grafted ramet above the graft union is genetically identical to the original plant (See also "Ramet, rooted.")
Ramet, rooted	A ramet created by rooting a twig or cutting from the original plant. The whole ramet is genetically identical to the original plant (See also, "Ramet, grafted.")
Reclamation	A planned series of activities designed to recreate the biophysical capacity of an ecosystem.
Reforestation	The reestablishment of trees on denuded forest land by natural or artificial means such as planting and seeding.
Registered lot number	See "Lot number, registered."
Registration	Process that allows a seed or vegetative lot to be used for *deployment* within its *deployment zone* or *seed zone*. Only *Stream 1* and *Stream 2 materials* can be registered. Registration may be *restricted* or *unrestricted*. A registered seed or vegetative lot is one that has completed the registration process.
Registration, unrestricted	See "Unrestricted registration."

Term	Definition
Registration, restricted	See "Restricted registration."
Research material, local	Seed or vegetative materials from within the target *breeding region* or an adjacent *breeding region* that may not be eligible for *registration* (e.g. an open-pollinated seedlot collected from a single tree). These materials may be included in a *controlled parentage program* leading to production of *Stream 2 material*. These materials must have an assigned *unique identifier* before being established in *genetic research plantings* or a *controlled parentage program*. The Breeding, Testing and Verification Standards apply to this material.
Research material, non-local	Seed or vegetative materials of unknown adaptation (such as species, provenance, family or hybrid material from outside the *seed zone* or *breeding region* of origin). Untested non-local research materials are not eligible for *deployment* within the *Green Area*, or inclusion in *production facilities* associated with *controlled parentage programs* (with some exceptions of material from adjacent *breeding regions*), but may be included in *genetic research plantings*. These materials must have an assigned *unique identifier* before being established in *genetic research plantings*. Following testing and demonstration of adaptedness, these materials may be included in *controlled parentage programs* leading to production of *Stream 2 materials*. The Breeding, Testing and Verification Standards apply to this material.
Restricted registration	Material registration category that does not allow unrestricted *deployment*. A limitation may be imposed on area or amount of material deployed, and/or monitoring requirements. Registration may be restricted for reasons of: • undetermined genetic or ecological risk • incomplete documentation, or • insufficient diversity levels, as indicated by *effective population size*, Ne.
Rolling front orchard	A *seed orchard* in which individual trees or groups of trees of known breeding value are replaced on a more or less continuous basis as new material of higher breeding value becomes available.
Seed orchard	A stand of trees, usually several hundred to several thousand in number, established and managed primarily for early and abundant production of seed for *deployment*. Trees in the orchard are derived and propagated from selected parent trees by grafting or by seed.
Seed zone	A geographic area, defined on the basis of ecological characteristics and genetic information, within which *Stream 1 material* meeting *unrestricted registration* requirements may be collected and freely deployed. Seed zones may apply to groups of species, or *species-specific* seed zones may be developed.
Serial propagation	The propagation of multiple clonal copies of a plant through repeated cycles of collection of vegetative units (e.g. scions or cuttings), creation of new plants from these units, and vegetative growth of the derived plants, without returning to the original plant. Also known as "bulking up" or multiplication.
Species-specific seed zone	A *seed zone*, delineated for a single species on the basis of adaptation as assessed from genetic *trials*, within which *Stream 1 material* may be collected and freely deployed.

Term	Definition
Stoolbed	An aggregation of closely spaced stumps, or stools, managed for the production of one-year-old vegetative sprouts (whips). Harvested whips are used for operational planting stock and can be pre-rooted prior to *deployment*.
Stream 1 material	Adapted seed or vegetative material collected from *wild* or artificially regenerated stands of native species within a given *seed zone*, having *restricted* or *unrestricted registration* for *deployment* in that *seed zone*. Adaptedness of Stream 1 material is assumed on the basis of limited geographic transfer from source location. Diversity and documentation standards apply. The Materials Collection, Handling, Registration and Storage Standards and the Green Area Deployment Standards apply to this material (see Appendix 6).
Stream 2 material	Adapted seed or vegetative material produced in a *production facility*, having *restricted* or *unrestricted registration* for *deployment* within the *deployment zone* of the associated *controlled parentage program*. Diversity and documentation standards apply. Adaptedness of Stream 2 material is assumed on the basis of limited geographic transfer from source location, or may be confirmed through long-term testing and/or monitoring, concurrent with use. Stream 2 material is derived from material collected within the target *deployment zone* or, in some cases, from adjacent areas or from material demonstrating adaptedness. Other material may be included in programs producing Stream 2 material following testing and demonstration of adaptedness (see "Research material, non-local"). All genetics policies apply to Stream 2 material (see Appendix 6).
Temporary lot number	See "Lot number, temporary."
Test	A *genetic research planting* designed to address a given genetic issue; may stand alone or may be one planting of a series including the same or overlapping material; e.g. a single progeny test site. Used interchangeably with *trial*.
Test series	A group of *genetic research plantings* of the same or overlapping material, on one or several sites, designed to address a given genetic issue; e.g. a progeny *test* established on four sites. Used interchangeably with trial series.
Trial	A *genetic research planting* designed to address a given genetic issue; may stand alone or may be one planting of a series including the same or overlapping material; e.g. a single progeny tria*l* site. Used interchangeably with *test*.
Trial series	A group of *genetic research plantings* of the same or overlapping material, on one or several sites, designed to address a given genetic issue; e.g. a progeny trial established on four sites. Used interchangeably with *test series*.
Unique identifier	An alphanumeric code of 7 to 13 characters assigned to genetic material. The first seven characters of the unique identifier are essential, and uniquely identify the *genotype* by agency and sequence number. Subsequent characters may be included as applicable, and specify material type (e.g. scions or pollen), individual number (e.g. cutting 103), and species (e.g. Sw). A unique identifier is required for all unregistered material included in research *trials* related to *controlled parentage programs*. See Appendix 25 for details of variables, structure and agency codes.
Unrestricted registration	Registration that allows a seed or vegetative lot to be used freely for *deployment* within its *deployment zone* or *seed zone*, without extraordinary monitoring requirements or other restrictions.

Term	Definition
Validated raw data	Raw data that has been examined and corrected for format, unambiguous errors and omissions, and credibility. Validation is now largely conducted during the data collection phase by programming the data logger to detect such anomalies as shrinking trees, trees that are too tall for the given Diameter at Breast Height (DBH) and live trees that were previously reported dead.
White Area	Private and *public land* in the settled portion of the province, managed primarily for agriculture use, but not excluding other uses such as timber, oil/gas development, recreation, soil and water conservation, and fish and wildlife habitat.
Wild	Genetic materials of native species originating from natural regeneration.

LIST OF ACRONYMS

AAC	Annual Allowable Cut
ARIS	Alberta Regeneration Information System
ATISC	Alberta Tree Improvement and Seed Centre
BTV	Breeding, Testing and Verification section of the standards
BV	Breeding Value
CNT	Consultative Notation
CPP	Controlled Parentage Program
DBH	Diameter at Breast Height
DFMP	Detailed Forest Management Plan
FHT	Fall Height measurement
FOIP	Freedom Of Information and Protection of Privacy Act
FMA	Forest Management Agreement
GAD	Green Area Deployment section of the standards
GMO	Genetically Modified Organism
GW	Genetic Worth
G&Y	Growth and Yield
ISP	Industrial Sample Plot designation
MCHRS	Material Collection, Handling, Registration and Storage section of the standards
MLL	Miscellaneous Lease
Ne	Effective population size
ODA	Ownership and Data Access section of the standards
OGR	Operating Ground Rules
PCPM	Production of Controlled Parentage Material section of the standards
PNT	Plant with Novel Traits
PST	Permanent Sample Tree
RP	Research Program
SRD	Sustainable Resource Development Department
TFA	Temporary Field Authority
TSA	Timber Supply Analysis
UTM	Universal Transverse Mercator

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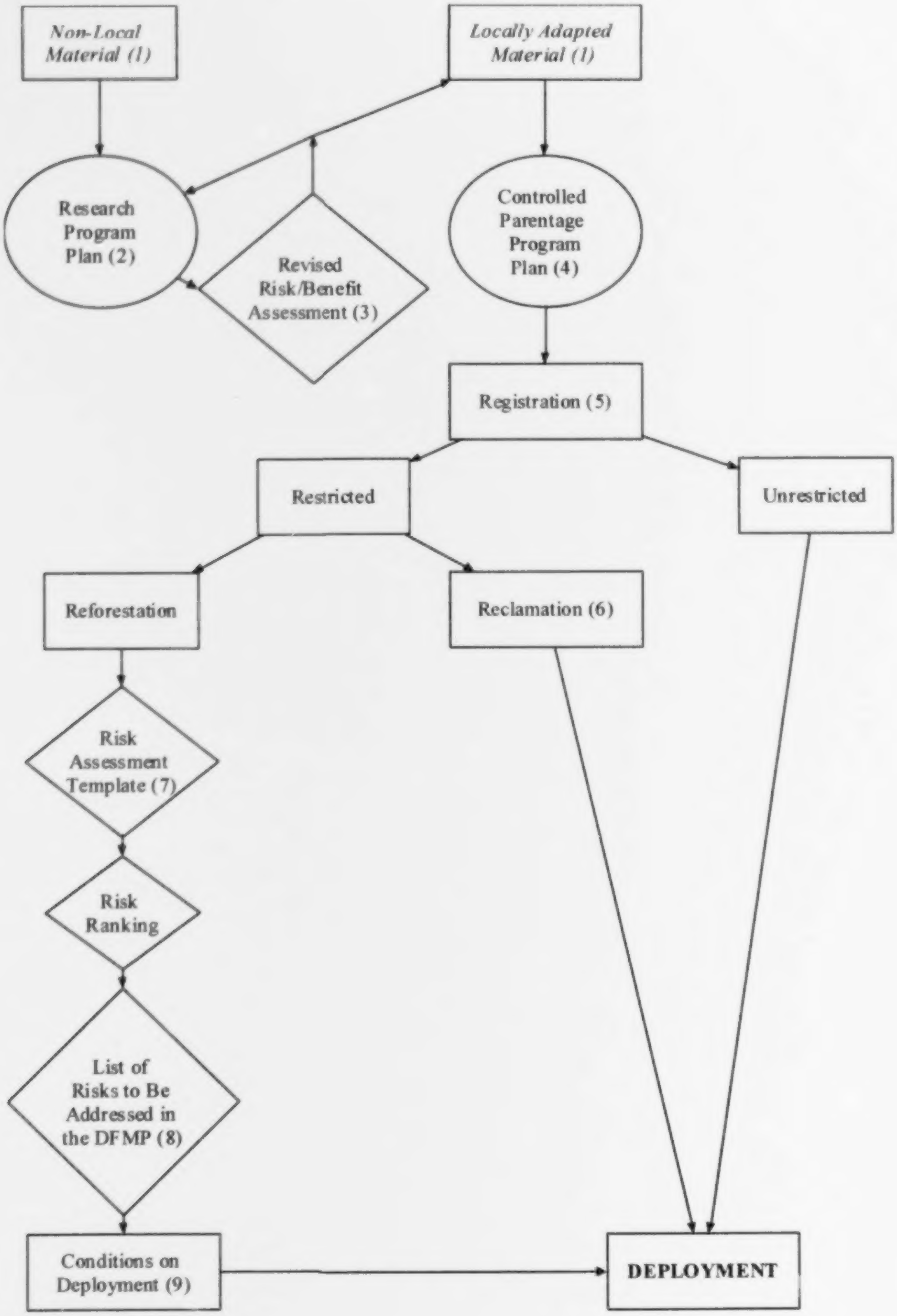
Appendix 1. Flow Diagram for Registration and Deployment of Stream 2 Material

See Standards 5.0, 18.4.1 and 25.1.



Non-Local Material (1)
Locally Adapted Material (1)
Research Program Plan (2)
Revised Risk/Benefit Assessment (3)
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Restricted
Unrestricted
Reforestation
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Risk Ranking
List of Risks to Be Addressed in the DFMP (8)
Conditions on Deployment (9)
DEPLOYMENT

Appendix 1 (continued). Flow Diagram for Registration and Deployment of Stream 2 Material

[1] See Glossary for definitions. Note that some material originally classified as having unproven adaptation may be considered to be locally adapted after research results are available.

[2] Appendix 24. Research Program Plan – Contents

[3] The risk/benefit assessment conducted as a part of the Research Plan will be revised on the basis of information resulting from implementation of the Research Plan.

[4] Appendix 18. Controlled Parentage Program Plan – Contents

[5] Appendices 4 and 5. Collection Requirements for Registration. Also, MCHRS standards.

[6] See Standards of the Department of Environment for *reclamation* plantings.

[7] Appendix 9. Assessment of Risk for Stream 2 Material

[8] Where "Classes of Risk" in the Risk Assessment Template are rated higher than "Low," the specific risks will be identified and listed in the DFMP.

[9] Options for accommodating risks include limits on area of *deployment*, establishment of buffers around plantations of restricted material, limits on the distance from where the wood will be used, requirements for an intermediate level ("pilot-scale") of *deployment* before *deployment* to specified area limits, agreements to prevent natural regeneration on areas occupied by material of *restricted registration*, etc.

Appendix 2. Registration Request Form - Stream 1

See Standards 10.1, 10.4, 10.6, 10.12, 12.3.1, 13.4, 13.5, 15.4.

ALBERTA SUSTAINABLE RESOURCE DEVELOPMENT

1. ADMINISTRATIVE INFORMATION

OWNER

ADDRESS

REGISTERED LOT NUMBER
ASSIGNED BY THE DEPARTMENT

SIMS INVENTORY NO.
FOR DEPARTMENT USE ONLY

REGISTRATION REQUEST
☐ UNRESTRICTED
☐ RESTRICTED
☐ PENDING REGISTRATION*

2. STAND AND SITE INFORMATION

SPECIES

ARIS CODE (see Appendix 6)

TEMPORARY LOT NUMBER
THE TEMPORARY LOT NUMBER IS ASSIGNED BY THE AGENCY AND MUST CORRESPOND WITH LABELLING ON SACKS, CONTAINERS, ETC.

ELEVATION RANGE (M) TO

SEED ZONE

LEGAL LOCATION (to legal sub-division)

PROVIDE EITHER LAT/LONG OR UTM INFORMATION BELOW:

UTM NORTHING	UTM EASTING
UTM NORTHING	UTM EASTING
UTM NORTHING	UTM EASTING
UTM NORTHING	UTM EASTING
LATITUDE ° ' "	LONGITUDE ° ' "
LATITUDE ° ' "	LONGITUDE ° ' "
LATITUDE ° ' "	LONGITUDE ° ' "
LATITUDE ° ' "	LONGITUDE ° ' "

3. COLLECTION INFORMATION

COLLECTION SUPERVISOR

COLLECTION METHOD

COLLECTION DATES

NO. OF TREES SAMPLED

CONTRACTOR

TYPE OF MATERIAL COLLECTED
AND TOTAL VOLUME AND/OR AMOUNTS COLLECTED

4. INTERIM STORAGE AND SHIPPING INFORMATION

INTERIM STORAGE DATES (INCLUDES COLD STORAGE)

DATE SHIPPED TO PROCESSING FACILITY

PROCESSING FACILITY

5. EXTRACTION AND CLEANING INFORMATION (TO BE COMPLETED BY PROCESSING FACILITY FOR SEED ONLY)

DATE RECEIVED	DATES EXTRACTED	AMOUNT CLEANED (KG)	SEED MOISTURE CONTENT

I HEREBY DECLARE THAT THE INFORMATION GIVEN ABOVE (SECTIONS 1, 2, 3, & 4) IS VALID AND CORRECT FOR THIS LOT.

NAME

POSITION

SIGNATURE

COMPANY

REMARKS

A COPY OF THIS FORM MUST ACCOMPANY MATERIAL TO PROCESSING AND/OR STORAGE FACILITIES IN COMPLIANCE WITH T/M REGULATION 144.3.

* Pending fulfillment of all requirements for registration, such as adequate number of trees sampled

INFORMATION FOR COMPLETING REGISTRATION REQUEST FORM – STREAM 1

All forest tree seed and vegetative materials to be used on *public land* must be registered with the Department. Completion of this form initiates the *registration* process for materials collected on *public land*. The agency or company doing the collection assigns a *temporary lot number*, writes it on the tag with the material, and completes the Registration Request Form. The Department assigns a *registered lot number* once *registration* is complete.

STAND AND SITE INFORMATION

ARIS Code

Choose the most appropriate category as listed in Appendix 6.

Temporary Lot Number

Assign the lot a temporary number to track the material during processing prior to *registration*. The *temporary lot number* must correspond with the tag on the lot containers, e.g. cone sacks.

Elevation

The range between maximum and minimum elevation values in metres.

Collection Site

Record the four most outside collection points to the degrees/minutes/seconds or UTMs. If the collection was made within a legal subdivision, then one collection point will be accepted.

COLLECTION INFORMATION

Collection method

Choose the single, most appropriate, collection method:

- Aerial
- Climbing
- Felled trees
- Ground, ladder and/or hydraulic lift
- Slash
- Squirrel cache

Also record the picking method:

- Hand picked
- Mechanically picked

EXTRACTION/CLEANING AND SHIPPING INFORMATION

Extraction information is to be completed by the processor. Moisture content is to be measured and recorded by the facility cleaning the seed. Only laboratory *test* results using International Seed Testing Association (ISTA) rules are acceptable and results must be expressed as a percentage by weight, calculated to one decimal place. (For seed testing guidelines see the Department's website).

Seed for shipping must be properly packaged to prevent transport damage. Each container must have a *temporary lot number* on a tag inside and one affixed to the outside.

REMARKS

Space is provided to record any additional stand, collection, handling or processing information.

Appendix 3. Registration Request Form - Stream 2

See Standards 10.1, 10.4, 10.9, 10.12, 12.4.1, 13.4, 13.5.

ALBERTA SUSTAINABLE RESOURCE DEVELOPMENT

1. ADMINISTRATIVE INFORMATION

TEMPORARY LOT NO. ____________________

REGISTERED LOT NO. ____________________

APPROVED BY THE DEPARTMENT

APPROVED FACILITY NO. ____________________

FACILITY LOCATION ____________________

SIMS INVENTORY NO. ____________________

FOR DEPARTMENT USE ONLY

REGISTRATION REQUEST

☐ UNRESTRICTED

☐ RESTRICTED

☐ PENDING REGISTRATION*

2. OWNERSHIP

COMPANY	% OF LOT ALLOCATED

3. GENETIC INFORMATION

SPECIES ____________________ DEPLOYMENT ZONE ____________________ GENETIC WORTH ____________________

EFFECTIVE POPULATION SIZE ____________________ ARIS CODE (see Appendix 6) ____________________

3. COLLECTION INFORMATION

COLLECTION SUPERVISOR ____________________

COLLECTION METHOD ____________________

COLLECTION DATES ____________________

CONTRACTOR ____________________

TYPE OF MATERIAL COLLECTED AND TOTAL VOLUME AND/OR AMOUNTS COLLECTED

4. INTERIM STORAGE AND SHIPPING INFORMATION

INTERIM STORAGE DATES (INCLUDES COLD STORAGE)

DATE SHIPPED TO PROCESSING FACILITY

PROCESSING FACILITY

5. EXTRACTION AND CLEANING INFORMATION (TO BE COMPLETED BY PROCESSING FACILITY FOR SEED ONLY)

DATE RECEIVED	DATES EXTRACTED	AMOUNT CLEANED (KG)	SEED MOISTURE CONTENT

THE ABOVE INFORMATION (SECTIONS 1, 2, 3, 4, & 5) WAS COMPLETED BY:

NAME ____________________ POSITION ____________________

SIGNATURE ____________________ COMPANY ____________________

REMARKS ____________________

A COPY OF THIS FORM MUST ACCOMPANY LOTS TO PROCESSING AND/OR STORAGE FACILITIES IN COMPLIANCE WITH T/M REGULATION 144.3

APPENDIX 4. COLLECTION REQUIREMENTS FOR REGISTRATION OF STREAM 1 MATERIAL

See Standards 10.4, 10.6, 10.8, 10.12, 11.4, 18.2.4, 20.2.

Requirements for *unrestricted registration* of *Stream 1 reforestation* seed or vegetative material destined for *deployment* on *Green Area public lands* are shown below. Some collections not meeting these requirements may be eligible for *restricted registration* (see Appendix 2). Lots that do not meet requirements for *restricted registration* (e.g. lots collected from fewer than the minimum number of trees specified below) may be collected and stored, pending fulfillment of *registration* requirements.

These guidelines and numerical limits on collection sizes were developed to safeguard genetic diversity by considering biological differences among species, patterns of natural variation, and quantitative implications of vegetative and sexual reproduction.

Material Category	**Stream 1 material**[1]	**Minimum trees per collection**[2] **for unrestricted registration**	**Maximum elevation range of trees collected from**[3]	**Maximum area from which collection is made**[4]	**Maximum amount of material per collection**
A	All seedlot collections except aspen	30	100 m	2 km radius[5]	See Appendix 14
B	Aspen seedlot collections	10 (well-spaced clones)	100 m	5 km radius[5]	See Appendix 14
C	Vegetative lots (deployed without serial propagation)	75[6]	100 m	5 km radius[5]	See Appendix 14
D	Vegetative lots (serial propagation before *deployment*)	120[6]	100 m	5 km radius[5]	See Appendix 14

[1] Proponents are encouraged to make *Stream 1* collections from *wild* stands within *in situ* conservation areas (see Standard 20.2) and adjoining areas to ensure that *wild* genetic resources are preserved.

[2] Lots from the same *seed zone* not meeting minimum standards for collection size may be combined to achieve required collection sizes for restricted or *unrestricted registration,* provided other registration requirements are met. For each of material categories A, B, C and D, lots collected from fewer than 20, 7, 75 and 75 trees respectively may be stored "pending *registration*" (see Appendix 2) and will only be registerable where so combined. Collection from numbers of trees between these numbers and the numbers shown in the table may be eligible for *restricted registration.*

[3] If collections span more than 100 m in elevational range, then *deployment* is limited to within the *seed zone* boundaries, and a request for *deployment* outside the *seed zone* of origin will not be approved.

[4] *Deployment* of collections made from an area larger than that described in this table will be limited to a total of 5 million seedlings/propagules per lot.

[5] If collections are made within the required radius in the table and within a 100 m elevational range, then material may be deployed up to 1 km outside the *seed zone* of origin, provided the difference in elevation from the point of collection to the point of *deployment* does not exceed 100 m. These collections are also eligible for movement outside of the seed zone of origin through application for a request for deployment variance for *Stream 1 material* (see Appendix 8).

[6] Must be collected from trees separated by at least 10 m.

APPENDIX 5. COLLECTION REQUIREMENTS FOR REGISTRATION OF STREAM 2 MATERIAL

See Standards 10.4, 10.9, 10.12.

Effective population size (Ne) requirements for *registration* of Stream 2 *reforestation* seed or vegetative material destined for *deployment* on *Green Area Public Lands*.

Stream 2 material	Ne (effective population size) [1,2]	Registration category	Maximum deployable numbers from a production facility
Seed lots	≥ 18 [1]	unrestricted	see Appendix 21
Vegetative lots	≥ 18 [1,2]	unrestricted	see Appendix 21
Seed lots	6 – 18[3]	restricted	see Appendices 1, 9 & 21
Vegetative lots	6 – 18[3]	restricted	see Appendices 1, 9 & 21
Seed lots	<6[3,4]	pending registration	0
Vegetative lots	<6[3,4]	pending registration	0

[1] See Appendix 36 for Ne calculation methods.

[2] For *dioecious* species, lots must derive from approximately equal numbers of male and female contributing clones.

[3] Lots with Ne < 18 may be combined to achieve threshold Ne levels of 6 and 18 for restricted and unrestricted registration respectively. Lots to be combined must be from a production facility targeting the same *deployment zone*.

[4] Lots with Ne < 6 may be held in interim storage, pending combination with other lot(s) to achieve registerable Ne levels.

Appendix 6. Stream Categories and ARIS Codes[1] for Genetic Material

See Standards 10.7, 10.11, 33.6, 34.5.

A. SEED

I. List of Potential Materials for Deployment on Provincial Public Land

	Material Type	Stream	ARIS Code
	a. Native seed collections from wild stands		
1.	Unselected parents from unselected stands	1	AIa1
2.	Unselected parents from selected stands	1	AIa2
3.	Selected parents from unselected stands	1	AIa3
4.	Selected parents from selected stands	1	AIa4
b.	**Native seed collections from artificially regenerated stands**		
5.	Unselected parents from unselected stands	1	AIb5
6.	Unselected parents from selected stands	1	AIb6
7.	Selected parents from unselected stands	1	AIb7
8.	Selected parents from selected stands	1	AIb8
c.	**Seed collections from production facilities [2]**		
9.	Improved orchard	2	AIc9
10.	Unimproved orchard	2	AIc10
11.	Seedlot with Ne<18 (*registration restricted*)[3]	2	AIc11
12.	*Hybrid orchard* [4]	2	AIc12
13.	*Non-local material*	2	AIc13
14.	*Genetically modified organisms (GMOs)*	2	AIc14

II. List of Potential Precursor Materials for Deployment on Provincial Public Land

a.	**Local seed**	
15.	Individual family	R
16.	Pollen	R
17.	GMOs	R
b.	**Non-local seed**	
19.	Provenances	R
20.	Species	R
21.	Hybrids	R
22.	Individual family	R
23.	*Genetically modified organisms (GMOs)*	R
24.	Pollen	R

Stream 1 = traditional *reforestation* stream (see glossary)
Stream 2 = *controlled parentage* stream (see glossary)
R = *research material* (see glossary)

---

[1] ARIS codes assigned only to *Stream 1 and 2 materials*; *research materials* cannot be deployed operationally.
[2] Orchards may include some trees from adjacent *breeding regions/deployment zones.*
[3] If material fits this category in addition to any other category, this category over-rides.
[4] Orchard designed to produce hybrid seed.

B. VEGETATIVE PROPAGULES

I. List of Potential Materials for Deployment on Provincial Public Land

	Material Type	Stream	ARIS Code
a.	**Native propagule collections from wild stands** [5]		
1.	Unselected parents from unselected stands	1	BIa1
2.	Unselected parents from selected stands	1	BIa2
3.	Selected parents from unselected stands	1	BIa3
4.	Selected parents from selected stands	1	BIa4
b.	**Native propagule collections from artificially regenerated stands**		
5.	Unselected parents from unselected stands	1	BIb5
6.	Unselected parents from selected stands	1	BIb6
7.	Selected parents from unselected stands	1	BIb7
8.	Selected parents from selected stands	1	BIb8
c.	**Propagules generated from production facilities**		
9.	Selected population	2	BIc9
10.	Tested population	2	BIc10
11.	Lot with Ne<18 (*registration restricted*)[6]	2	BIc11
12.	*Amplified family*	2	BIc12
13.	Hybrids [7]	2	BIc13
14.	*Non-local material*	2	BIc14
15.	*GMOs*	2	BIc15

II. List of Potential Precursor Materials for Deployment on Provincial Public Land

a.	**Local material**	
16.	Individual family	R
17.	Individual clones	R
18.	Pollen	R
19.	GMOs	R
b.	**Non-local material**	
20.	Provenance material	R
21.	Species material	R
22.	Hybrid material	R
23.	Individual clones	R
24.	Pollen	R
25.	GMOs	R

Stream 1 = traditional *reforestation* stream (see glossary)
Stream 2 = controlled parentage stream (see glossary)
R = *research material* (see glossary)

---

[5] Materials may be multiplied in *stoolbeds* that meet the minimum number of trees required per collection for *Stream 1 material* (see Standard 11.4 and Appendix 4).

[6] If material fits this category in addition to any other category, this category over-rides.

[7] Hybrid with at least one non-local parent

Appendix 7. Seed Zone Descriptions, Areas and Maps

See Standards 10.8, 18.2.1, 20.2.

Populations of forest tree species exhibit genetic variation associated with differences in the geography and climate of origin. Such variation is the result of long-term evolutionary processes and is key to biological adaptation to regional habitats and to maintenance of future evolutionary potential. For these reasons, movement of all seed to *reforestation* sites on *public land* is regulated.

Seed Zones

A seed zonation system for Alberta has been developed for natural seed movement and will replace the existing Seed Provenance Rule (*deployment* within a 50 mile radius and plus/minus 500 feet elevation movement from location of collection). *Seed zones* are geographic subdivisions of Natural Regions and are based on general genetic criteria. They limit seed movement to a conservative area where native trees of all species can be moved without risk of mal-adaptation or erosion of genetic integrity. Seed collections from natural stands of all species within a *seed zone* meeting *unrestricted registration* requirements can be moved without restriction. There are a total of 84 described *seed zones* for Alberta, which cover all species and areas of the province with the exception of the mountain National Parks. Seventy-four *seed zones* are applicable to the *Green Area*.

The Forestry Seed Zones of Alberta are delineated for all areas of Alberta (with the exception of the mountain National Parks) and are inclusive for all native forest plant species. The intent of *seed zones* is to provide delineated ecological land units within which planning, collection, inventory maintenance, conservation and *deployment* can occur for reproductive materials of natural forest plant species, with emphasis on tree species.

Seed zone delineation is hierarchical, and based on Alberta's six Natural Regions, their Natural Subregions and Ecodistricts. Where there was a concern that the Natural Regions, Subregions or Ecodistricts did not adequately capture natural adaptive genetic variation, elevation contours were used for further subdivision.

Seed zone numbering and naming progresses from north to south generally, and from north to south and from lower to higher elevations within Natural Regions. *Seed zone* names incorporate both ecological and physiological features. The *seed zones* are listed in Table 1 and mapped in Figures 1 and 2.

Seed zone delineation will be periodically reviewed and updated to incorporate any significant boundary changes to the Natural Regions, Natural Subregions or Ecodistricts.

For larger scale maps, contact the Land and Forest Division of the Department.

Table 1. Seed Zone Numbers, Areas and Names

Natural Regions of Alberta	Seed Zone	Seed Zone Area (ha)	Seed Zone Name
Boreal Forest Natural Region	B1.1	3,330,000	Hay River Wetland Mixedwood Lowlands
	B2.1	1,030,000	Peace River Central Mixedwood Delta Plain
	B3.1	980,000	Northern Great Slave Central Mixedwood Plain
	B3.2	1,470,000	Southern Great Slave Central Mixedwood Plain
	B4.1	2,000,000	Loon Lake and Mikkwa Central Mixedwood Lowlands
	B4.2	1,140,000	Mackay Central Mixedwood Lowlands
	B4.3	1,850,000	Wabasca Central Mixedwood Lowlands
	B5.1	1,570,000	Saskatchewan Central Mixedwood Plain
	B6.1	2,190,000	Mostoos Hills Central Mixedwood Uplands
	B6.2	1,260,000	Lesser Slave and Tawatinaw Central Mixedwood Plain
	B7.1	150,000	Utikuma Central Mixedwood Uplands
	B8.1	780,000	Wapiti Central Mixedwood Uplands
	B9.1	1,860,000	Vermillion Dry Mixedwood Lowlands
	B9.2	1,700,000	Northern Peace Dry Mixedwood Lowlands
	B9.3	2,010,000	Southern Peace Dry Mixedwood Lowlands
	B10.1	2,120,000	Lac La Biche Dry Mixedwood Plain
	B10.2	1,580,000	Red Water Dry Mixedwood Plain
	B10.3	820,000	Foothills Dry Mixedwood Uplands
	B11.1	280,000	Cameron Hills Mixedwood Highlands
	B11.2	310,000	Zama Ridge and Basset Hill Mixedwood Highlands
	B11.3	430,000	Caribou Mountains and Watt Mountain Mixedwood Highlands
	B11.4	590,000	Buffalo Head Hills Mixedwood Highlands
	B11.5	830,000	Birch Mountains Mixedwood Highlands
	B12.1	200,000	Stony Mountain Highlands
	B13.1	180,000	Buffalo Head Hills Coniferous Highlands
	B13.2	740,000	Birch Mountains Coniferous Highlands
	B14.1	550,000	Bistcho Lake Sub-Arctic Plain
	B14.2	310,000	Cameron Hills Sub-Arctic Uplands
	B14.3	930,000	Caribou Mountains Sub-Arctic Uplands
	B14.4	260,000	Birch Mountains Sub-Arctic Uplands
Parkland Natural Region	P1.1	480,000	Peace River Parkland Lowland
	P2.1	5,350,000	Central Parkland Plains
	P3.1	410,000	Rocky Mountain Foothills Parkland
Canadian Shield Natural Region	C1.1	880,000	Kazan Uplands
	C2.1	680,000	Athabasca Plain

Natural Regions of Alberta	Seed Zone	Seed Zone Area (ha)	Seed Zone Name
Foothills Natural Region	F1.1	2,110,000	Clear Hills Lower Foothills
	F2.1	260,000	Saddle Hills Lower Foothills
	F2.2	1,020,000	Grande Cache-Summit Lower Foothills
	F3.1	1,000,000	Swan Hills Lower Foothills
	F3.2	250,000	Pelican Mountains Lower Foothills
	F4.1	1,260,000	Drayton Lower Foothills
	F5.1	700,000	Wolf Lake Lower Foothills
	F5.2	360,000	O'Chiese Lower Foothills
	F6.1	110,000	Little Red Deer Lower Foothills
	F6.2	160,000	Bragg Creek Lower Foothills
	F7.1	1,140,000	Clear Hills Upper Foothills
	F8.1	1,010,000	Grande Cache Upper Foothills
	F8.2	110,000	Mayberne Upper Foothills
	F9.1	230,000	Swan Hills Upper Foothills
	F10.1	390,000	Coal Branch Upper Foothills
	F11.1	160,000	Clearwater Upper Foothills
	F11.2	180,000	Red Deer Upper Foothills
Rocky Mountain Natural Region	M1.1	20,000	Grande Cache Montane
	M2.1	10,000	Athabasca Valley Montane
	M3.1	40,000	North Saskatchewan Valley Montane
	M4.1	5,000	Ya Ha Tinda Montane
	M5.1	100,000	Bow Valley Montane
	M6.1	60,000	Cypress Hills Montane
	M7.1	240,000	Crowsnest-Livingston Montane
	M7.2	N/A	Porcupine Hills Montane
	M8.1	30,000	Castle-Waterton Montane
	LS1.1	500,000	Grande Cache Lower Sub-Alpine
	LS2.1	240,000	Athabasca-North Saskatchewan Lower Sub-Alpine
	LS3.1	190,000	North Saskatchewan-Clearwater Lower Sub-Alpine
	LS3.2	40,000	Clearwater-Bow Lower Sub-Alpine
	LS4.1	380,000	Kananaskis-Highwood Lower Sub-Alpine
	LS4.2	N/A	Livingston-Crowsnest Lower Sub-Alpine
	LS5.1	N/A	Castle-Waterton Lower Sub-Alpine
	US1.1	220,000	Northern Upper Sub-Alpine
	US2.1	150,000	Athabasca-North Saskatchewan Upper Sub-Alpine
	US3.1	130,000	North Saskatchewan-Bow Upper Sub-Alpine
	US4.1	N/A	Kananaskis-Highwood Upper Sub-Alpine
	US4.2	N/A	Wilkinson-Crowsnest Upper Sub-Alpine
	US5.1	N/A	Castle-Waterton Upper Sub-Alpine
	A1.1	190,000	Grande Cache-Hinton Alpine
	A2.1	150,000	Athabasca-North Saskatchewan Alpine
	A3.1	140,000	North Saskatchewan-Bow Alpine
	A4.1	N/A	Bow-Crowsnest Alpine
	A5.1	N/A	Crowsnest-Waterton Alpine
Grassland Natural Region	G1.1	1,540,000	Northern Plains Fescue Grassland
	G2.1	1,490,000	Foothills Fescue Grassland
	G3.1	1,620,000	Western Alberta Plains Mixedgrass Grasslands
	G3.2	300,000	Cypress Hills Upland Mixedgrass Grassland
	G4.1	4,710,000	Eastern Alberta Plains Dry Mixedgrass Grassland

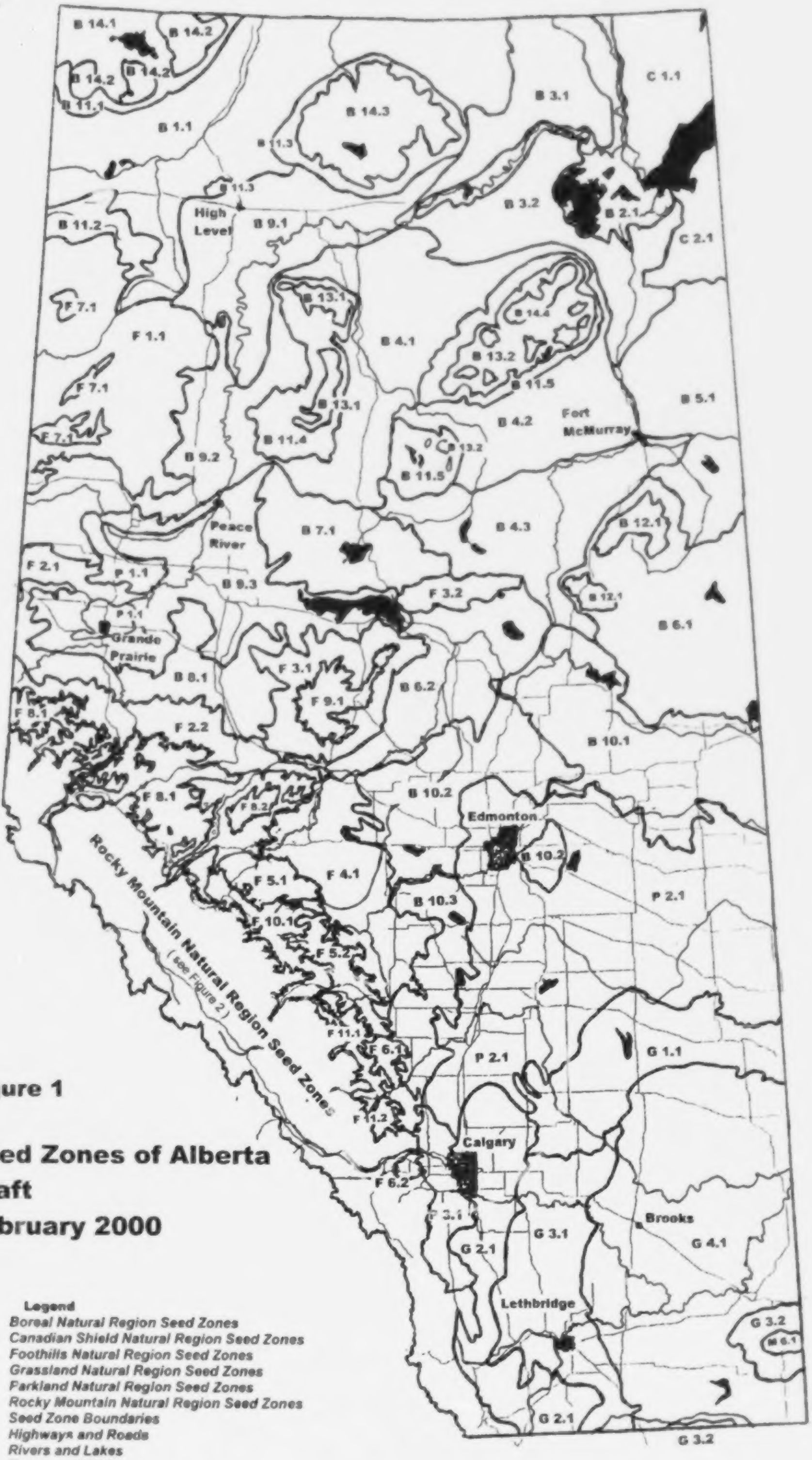

B 14.1
B 14.2
B 14.2
B 14.2
B 11.1
B 1.1
B 11.3
B 14.3
B 3.1
C 1.1
B 11.3
High Level
B 9.1
B 11.2
B 3.2
B 2.1
C 2.1
F 7.1
F 1.1
B 13.1
B 4.1
B 14.4
B 13.2
B 11.5
F 7.1
B 13.1
B 4.2
Fort McMurray
B 5.1
F 7.1
B 11.4
B 9.2
B 13.2
B 11.5
Peace River
B 7.1
B 4.3
B 12.1
F 2.1
P 1.1
B 9.3
F 3.2
B 12.1
P 1.1
Grande Prairie
B 6.1
F 3.1
B 8.1
F 9.1
B 6.2
F 8.1
F 2.2
B 10.1
F 8.1
F 8.2
B 10.2
Edmonton
B 10.2
Rocky Mountain Natural Region Seed Zones
(see Figure 2)
F 5.1
F 4.1
B 10.3
P 2.1
F 10.1
F 5.2
F 11.1
F 6.1
P 2.1
G 1.1
F 11.2
Calgary
F 6.2
P 3.1
G 3.1
Brooks
G 4.1
G 2.1
Lethbridge
G 3.2
M 6.1
G 2.1
G 3.2

Figure 1

Seed Zones of Alberta
Draft
February 2000

Legend
B Boreal Natural Region Seed Zones
C Canadian Shield Natural Region Seed Zones
F Foothills Natural Region Seed Zones
G Grassland Natural Region Seed Zones
P Parkland Natural Region Seed Zones
R Rocky Mountain Natural Region Seed Zones
Seed Zone Boundaries
Highways and Roads
Rivers and Lakes
Towns and Cities

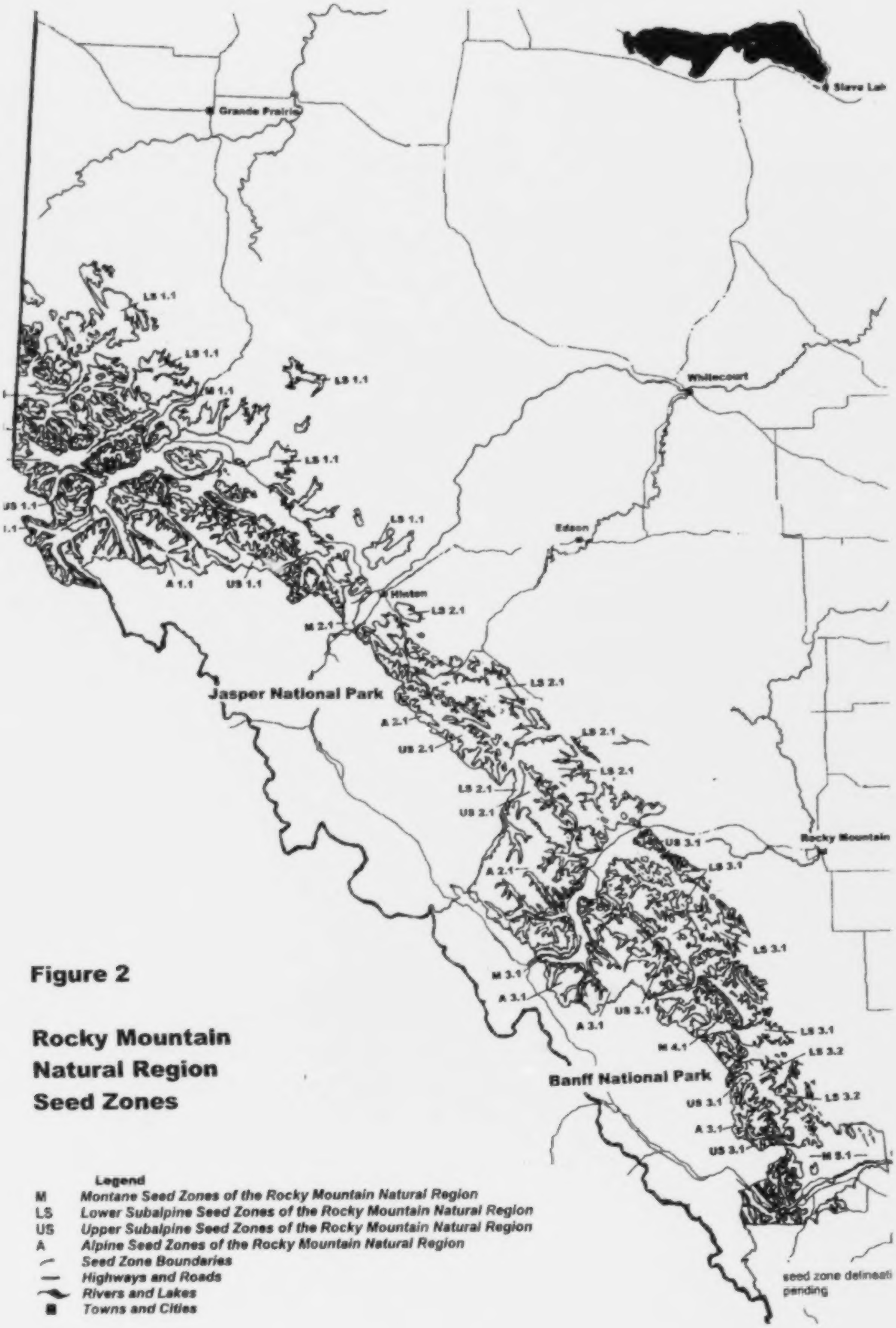

Slave Lak
Grande Prairie
LS 1.1
LS 1.1
LS 1.1
M 1.1
LS 1.1
US 1.1
1.1
LS 1.1
A 1.1
US 1.1
Whitecourt
Edson
Hinton
LS 2.1
M 2.1
LS 2.1
Jasper National Park
A 2.1
US 2.1
LS 2.1
LS 2.1
LS 2.1
US 2.1
US 3.1
Rocky Mountain
LS 3.1
A 2.1
LS 3.1
M 3.1
A 3.1
US 3.1
A 3.1
LS 3.1
M 4.1
LS 3.2
Banff National Park
US 3.1
LS 3.2
A 3.1
US 3.1
M 5.1
seed zone delineati
pending
Legend
M Montane Seed Zones of the Rocky Mountain Natural Region
LS Lower Subalpine Seed Zones of the Rocky Mountain Natural Region
US Upper Subalpine Seed Zones of the Rocky Mountain Natural Region
A Alpine Seed Zones of the Rocky Mountain Natural Region
Seed Zone Boundaries
Highways and Roads
Rivers and Lakes
Towns and Cities

Figure 2

Rocky Mountain
Natural Region
Seed Zones

Appendix 8. Request for Deployment Variance for Stream 1 Material

See Standards 10.13, 11.2, 18.2.4, 18.2.5, 18.2.6.

DATE ____________

REQUESTING AGENCY

Agency Name ____________ Contact ____________

Mailing Address ____________

____

____

Phone ____________ Fax ____________

E-mail ____________

REQUEST CATEGORY

Lot has restricted registration ____ and/or Transfer outside seed zone of origin ____

TYPE OF VARIANCE REQUESTED

Annual ____________ Standing ____________

Species ____________ Category of Material ____________

REASONS FOR REQUEST (Include Standards not met) ____________

____

____

____

CROP DESCRIPTION

Registered Lot Number ____________ Seed ____________ Vegetative ____________

Seed Zone ____________ Crop size ____________

Latitude ____________ Elevation: Mean ____________

Longitude ____________ Elevation: Range ____________

Legal Location ____________ UTM Northing ____________

UTM Easting ____________

PROPOSED DEPLOYMENT

Seed Zone ____________

Latitude ____________ Elevation: Mean ____________

Longitude ____________ Elevation: Range ____________

Legal Location ____________ UTM: Northing ____________

UTM: Easting ____________

Years of Deployment ____________ Total Number of Seedlings or Propagules ____________

MONITORING AND REPORTING SCHEDULE ____________

____

____

PROPONENT/AGENCY

Name ____________ Title ____________

Signature ____________ Date ____________

Appendix 9. Assessment of Risk for Stream 2 Material

See Standards 10.13, 18.4.1, 18.4.7, 22.2, 24.4.1.

When required, appropriate tables are to be developed jointly by the proponent and the Department. Following the assessment, the proponent is to include in its DFMP management strategies for Risk Classes scored as greater than "Low."

Assessment of Risk for Stand Level, Mixed Distribution Stream 2 Materials

Level:[8] **Stand** _X_ **Distribution:**[9] **Mixed** _X_
Landscape __ **Clonal** ___

Species	Category of Material[10]	Effective Population Size	Origin of Material[11]	Classes of Risk[12]			
				Sustain-ability[13]	Genetic Diversity[6]	Ecosystem Impact[6]	Management Impact[6]
White spruce, black spruce, lodgepole pine, jack pine and Douglas-fir	Seed	>18	Locally Adapted	N/A	N/A	N/A	N/A
	Seed	12 to 18	Locally Adapted	VL+	VL+	VL	VL+
	Seed	6 to 12	Locally Adapted	L+	M	VL+	L+

Assessment of Risk for Landscape Level, Mixed Distribution Stream 2 Materials

Level:[1] **Stand** ___ **Distribution:**[2] **Mixed** _X_
Landscape _X_ **Clonal** ___

Species	Category of Material[3]	Effective Population Size	Origin of Material[4]	Classes of Risk[5]			
				Sustain-ability[6]	Genetic Diversity[6]	Ecosystem Impact[6]	Management Impact[6]
White spruce, black spruce, lodgepole pine, jack pine and Douglas-fir	Seed	>18	Locally Adapted	N/A	N/A	N/A	N/A
	Seed	12 to 18	Locally Adapted	L	L+	L	L+
	Seed	6 to 12	Locally Adapted	M	M+	M	M

---

[1] "Level" is the size of area for which risks are to be considered; "Stand" refers to an isolated cutblock of average size; "Landscape" refers to the aggregate effect of stands over an area of 10,000 ha, more or less.

[2] "Distribution" is the degree of mixing of different *genotypes*. "Mixed" refers to thorough mixtures of planting stock; "Family/Clonal Blocks" refers to planting of one family or clone.

[3] "Category of material" is seed or vegetative material.

[4] "Origin of material": locally *adapted*, hybrid, non-local or *GMO*.

[5] "Classes of risk" represent groupings of several types of risk.
"Sustainability" refers to risks to sustained productivity from inbreeding associated with reduced numbers of parents and to reduced seeding potential when *dioecious* species are deployed in clonal blocks.
"Genetic diversity" represents potential impacts of reduced genetic diversity, including increased genetic vulnerability to pests and weather effects, genetic recombination in hybrids and reduced evolutionary potential.
"Ecosystem impact" includes potential of improved plantings to serve as centres for pest dispersal, weediness, gene flow and impacts on non-target species.
"Management impact" includes patterns of distribution of material (scattered or clustered), location (in relation to mills or tree improvement facilities) and expected intensity of silviculture associated with deployment.

[6] For relevant combinations of species, category of material, minimum effective population and origin of material, perceived risk is scored as "Very Low (VL)", "Low (L)", "Medium (M)", "High (H)" or "Very High (VH)" for each of the four classes of risk. Where scores are greater than "Low," the specific risks and proposals for their management are required in the DFMP.

Template for Assessment of Restricted Registration Materials

This template is a generic form to be applied to all materials with *restricted registration*. It is to be applied at the stand and landscape levels as well as for plantings where seedlings or vegetative material are deployed as mixes or where materials are proposed for *deployment* as single clones or single-family blocks.

Level:[1] **Stand** ___ **Distribution:**[2] **Mixed** ___
Landscape ___ **Clonal** ___
Stream 1 ___ **or Stream 2** ___

Species	Category of Material[3]	Effective Population Size	Origin of Material[4]	Classes of Risk[5]			
				Sustain-ability[6]	Genetic Diversity[6]	Ecosystem Impact[6]	Management Impact[6]

[1] "Level" is the size of area for which risks are to be considered; "Stand" refers to an isolated cutblock of average size; "Landscape" refers to the aggregate effect of stands over an area of 10,000 ha, more or less.

[2] "Distribution" is the degree of mixing of different *genotypes*. "Mixed" refers to thorough mixtures of planting stock; "Family/Clonal Blocks" refers to planting of one family or clone.

[3] "Category of material" is seed or vegetative material.

[4] "Origin of material": locally *adapted*, hybrid, non-local or *GMO*.

[5] "Classes of risk" represent groupings of several types of risk.

"Sustainability" refers to risks to sustained productivity from inbreeding associated with reduced numbers of parents and to reduced seeding potential when *dioecious* species are deployed in clonal blocks.

"Genetic diversity" represents potential impacts of reduced genetic diversity, including increased genetic vulnerability to pests and weather effects, genetic recombination in hybrids and reduced evolutionary potential.

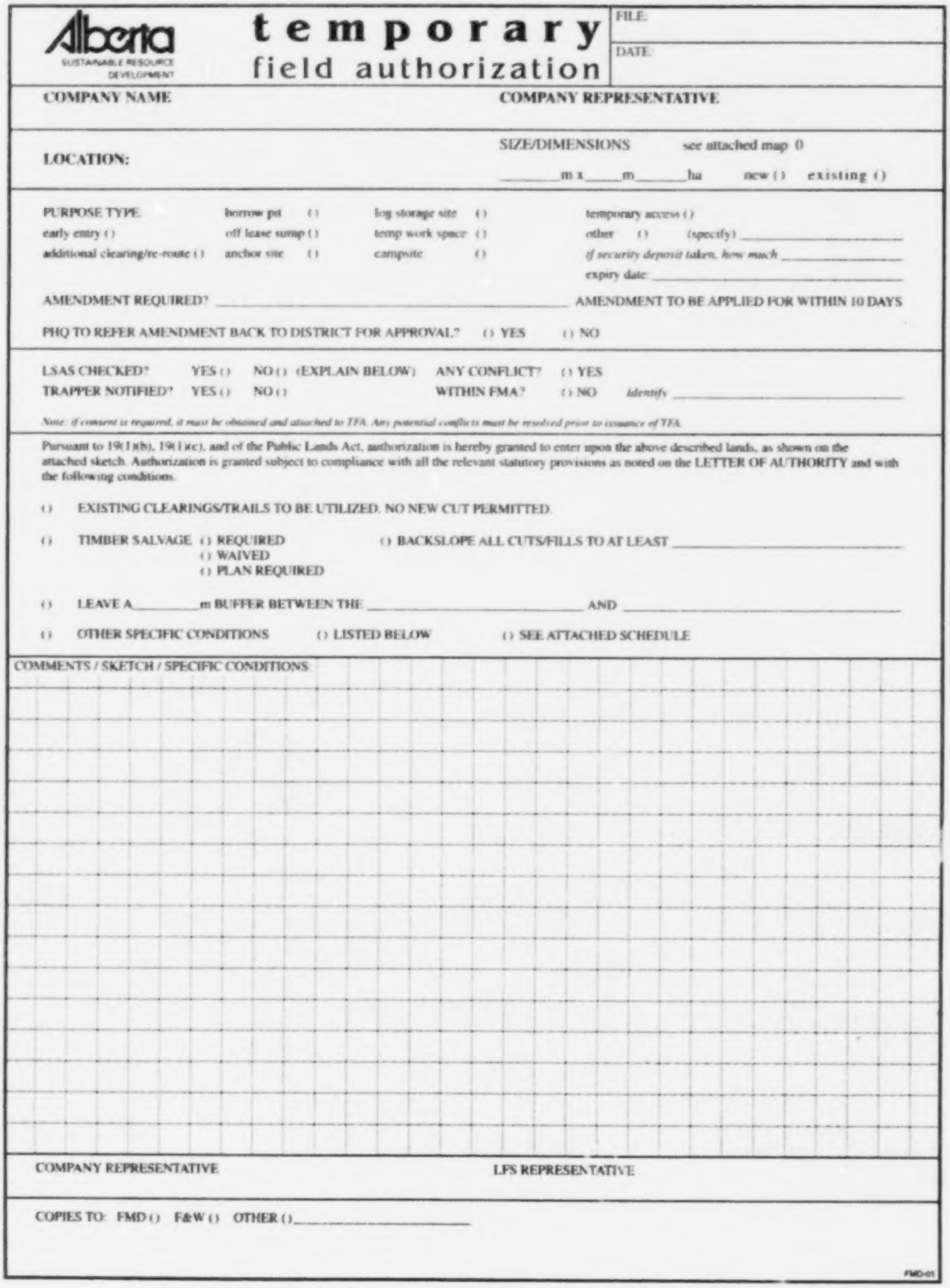
"Ecosystem impact" includes potential of improved plantings to serve as centres for pest dispersal, weediness, gene flow and impacts on non-target species.

"Management impact" includes patterns of distribution of material (scattered or clustered), location (in relation to mills or tree improvement facilities) and expected intensity of silviculture associated with deployment.

[6] For relevant combinations of species, category of material, minimum effective population and origin of material, perceived risk is scored as "Very Low (VL)", "Low (L)", "Medium (M)", "High (H)" or "Very High (VH)" for each of the four classes of risk. Where scores are greater than "Low," the specific risks and proposals for their management are required in the DFMP.

Appendix 10. Temporary Field Authorization Form

See Standard 11.1.3.



Alberta
SUSTAINABLE RESOURCE DEVELOPMENT

temporary field authorization

FILE:

DATE:

COMPANY NAME | **COMPANY REPRESENTATIVE**

LOCATION:

SIZE/DIMENSIONS see attached map ( )

________m x_____m_______ha new ( ) existing ( )

PURPOSE TYPE:
early entry ( )
additional clearing/re-route ( )

borrow pit ( )
off lease sump ( )
anchor site ( )

log storage site ( )
temp work space ( )
campsite ( )

temporary access ( )
other ( ) (specify) ____________
if security deposit taken, how much ____________
expiry date: ____________

AMENDMENT REQUIRED? ____________ AMENDMENT TO BE APPLIED FOR WITHIN 10 DAYS

PHQ TO REFER AMENDMENT BACK TO DISTRICT FOR APPROVAL? ( ) YES ( ) NO

LSAS CHECKED? YES ( ) NO ( ) (EXPLAIN BELOW) ANY CONFLICT? ( ) YES

TRAPPER NOTIFIED? YES ( ) NO ( ) WITHIN FMA? ( ) NO *identify* ____________

Note: if consent is required, it must be obtained and attached to TFA. Any potential conflicts must be resolved prior to issuance of TFA.

Pursuant to 19(1)(b), 19(1)(c), and of the Public Lands Act, authorization is hereby granted to enter upon the above described lands, as shown on the attached sketch. Authorization is granted subject to compliance with all the relevant statutory provisions as noted on the LETTER OF AUTHORITY and with the following conditions.

( ) EXISTING CLEARINGS/TRAILS TO BE UTILIZED. NO NEW CUT PERMITTED.

( ) TIMBER SALVAGE ( ) REQUIRED
( ) WAIVED
( ) PLAN REQUIRED

( ) BACKSLOPE ALL CUTS/FILLS TO AT LEAST ____________

( ) LEAVE A________m BUFFER BETWEEN THE ____________ AND ____________

( ) OTHER SPECIFIC CONDITIONS ( ) LISTED BELOW ( ) SEE ATTACHED SCHEDULE

COMMENTS / SKETCH / SPECIFIC CONDITIONS:

COMPANY REPRESENTATIVE | LFS REPRESENTATIVE

COPIES TO: FMD ( ) F&W ( ) OTHER ( )____________

FMD-01

APPENDIX 11. PARENT TREE SELECTION FORM – WILD STANDS AND PLANTATIONS

See Standards 11.1.5, 25.5, 26.1.

Species ____________________ ***Field Number*** ______________ ***Unique Identifier*** ____________________
Selection Agency ____ ***Selection Date*** ____________________

STAND INFORMATION

Collection Site____________________________ Natural Subregion ____________________
Legal Location____________________________ Seed Zone____________________
Latitude____________________________ Site Type____________________
Longitude____________________________ Stand Type____________________
Elevation____________________________ Moisture Regime____________________

Stand Comments: ____

TREE INFORMATION

Sex	Male ☐	Female ☐	*Monoecious* ☐	
Wood Sample	YES ☐	NO ☐	Collection Date_	
Scions	YES ☐	NO ☐	Collection Date_	
Open Pollinated Seed	YES ☐	NO ☐	Collection Date_	

Trait	**SELEC T TREE**	**Dom.[1] 1**	**Dom.[1] 2**	**Dom.[1] 3**	**Superiority[1] (%)**	**Comments**
Height (m)						
Natural Pruning (%)						
Height/Age (cm/yr)						
DBH (cm)						
Radial Increment						
Last 10 yrs (mm)						
Last 11-20 yrs (mm)						
Stem Form						
Branch Angle						
Branch Thickness						
Crown Width						

[1] Dominant tree data required when making selections using the comparison tree method

TREE REMARKS ____

Parent Tree Location Map	**Description**
	Location/Access Tree Marking: Photo Attached YES ☐ NO ☐

AGENCY REPRESENTATIVE ____________________ Signature ____________________ Date ______________

Appendix 12. Parent Tree Selection Form – Genetic Tests

See Standards 11.1.5, 25.5, 26.1.

Species ____________

Collector ____________

Unique Identifier ____________

Selection Date ____________

Collection Agency ____________

SELECTION SITE

Site ID ____________

Site Name ____________

Elevation (m) ____________

Legal Location ____________

____

Trial Code ____________

Latitude ____________

Longitude ____________

UTM Northing ____________

UTM Easting ____________

SELECTED TREE LOCATION

Selected Tree Field Number # ____________

Rep. # ____________

Row # ____________

Seedlot # ____________

Set or Block # ____________

Position # ____________

SELECTION INFORMATION

Sex Male ☐ Female ☐ *Monoecious* ☐

Selection Criteria or Report ____________

____

Purpose of Selection ____________

____

Age at Measurement ____________

Traits	Data	Comments
Height (m)		
DBH (cm)		
(other measured traits below)		
Pest Damage		

INFORMATION ON PARENTS OF THIS SELECTION

Breeding Date ____________

Mother ____________

Unique Identifier/ ____________

Genetic Identity ____________

Breeding Region ____________

Seed Zone ____________

Deployment Zone ____________

Origin ____________

Latitude ____________

Longitude ____________

Elevation ____________

Father ____________

Unique Identifier/ ____________

Genetic Identity ____________

Breeding Region ____________

Seed Zone ____________

Deployment Zone ____________

Origin ____________

Latitude ____________

Longitude ____________

Elevation ____________

GENERAL REMARKS

____

____

AGENCY REPRESENTATIVE ____________

____

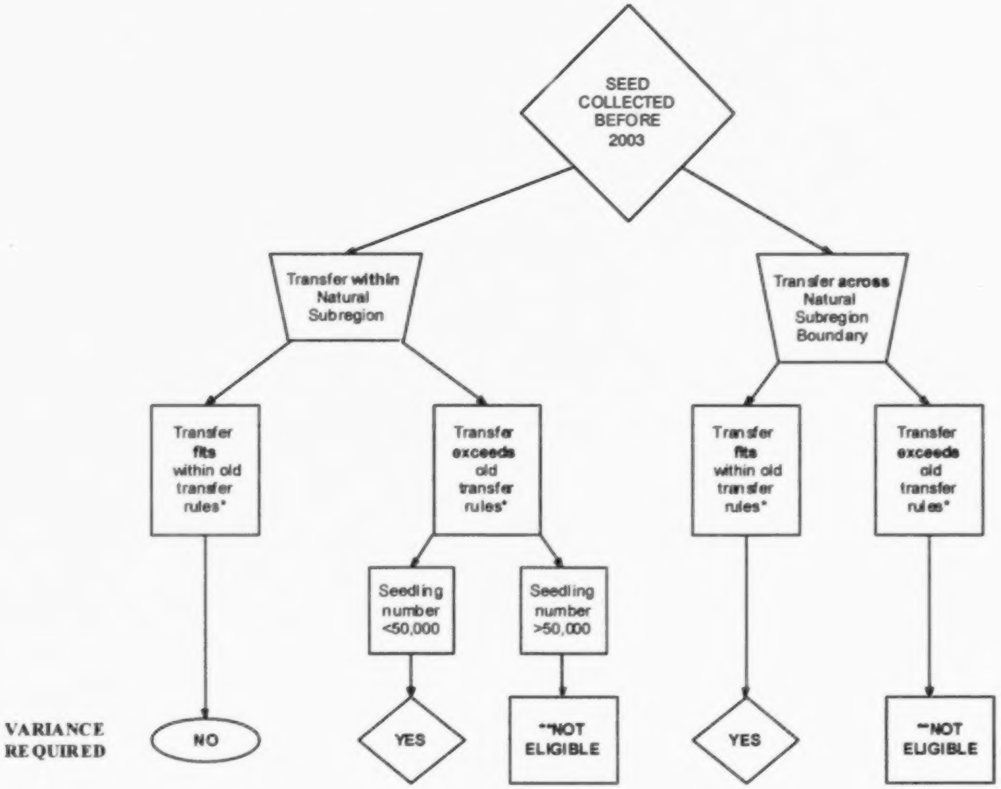
Signature ____________

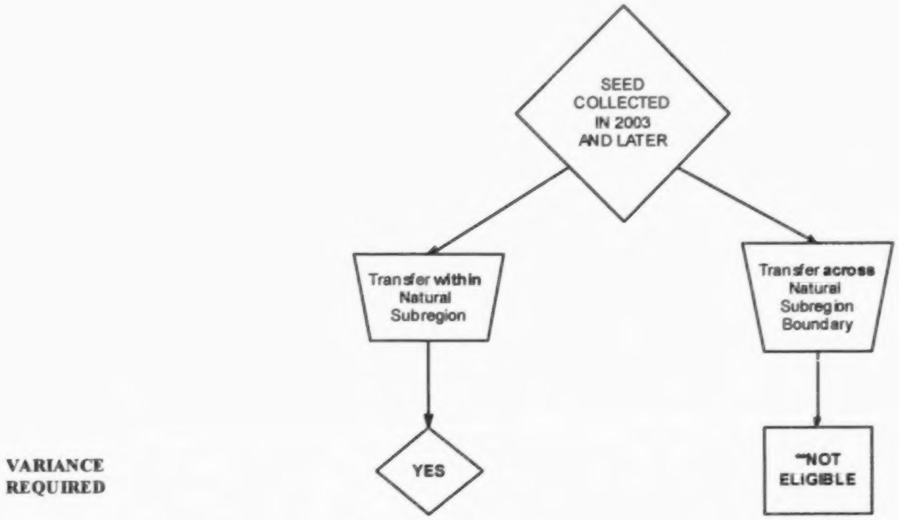
Date ____________

Photo of selected tree attached ☐

Appendix 13. Decision Tree for Transfer of Stream 1 Material Outside Seed Zone of Origin

See Standards 11.2, 18.2.2, 18.2.4.


SEED COLLECTED BEFORE 2003
Transfer within Natural Subregion
Transfer across Natural Subregion Boundary
Transfer fits within old transfer rules*
Transfer exceeds old transfer rules*
Transfer fits within old transfer rules*
Transfer exceeds old transfer rules*
Seedling number <50,000
Seedling number >50,000
VARIANCE REQUIRED
NO
YES
**NOT ELIGIBLE
YES
**NOT ELIGIBLE


SEED COLLECTED IN 2003 AND LATER
Transfer within Natural Subregion
Transfer across Natural Subregion Boundary
VARIANCE REQUIRED
YES
**NOT ELIGIBLE

* "Old transfer rules" refers to deployment within 50 miles and within 500 feet elevation from the collection location.

** Transfers classified as "not eligible" for a variance request may be considered in emergencies.

Appendix 14. Stream 1 Seedling and Vegetative Propagule Lot Deployment Limit by Seed Zone

See Standards 11.3, 18.2.3, 18.2.4.

Size Category	Seed Zone Area (ha)[1]	Maximum Number Deployable per Lot[2]		Approximate kg Seed[3]			Approximate Coverage in ha (@1800/ha)	
		Seedlings	Vegetative Propagules	Sw	Aw	Pl	Seedlings	Vegetative Propagules
1	> 1 million	25 million	20 million	150	6.1	250	13,888	11,110
2	500,000 to 1 million	20 million	16 million	120	4.9	200	11,111	8,889
3	100,000 to 500,000	15 million	12 million	90	3.7	150	8,333	4,167
4	< 100,000	10 million	8 million	60	2.4	100	5,555	2,778

[1] Refer to Appendix 7 for *seed zone* sizes.

[2] *Deployment* limit includes seed and vegetative propagules from a single lot.

[3] Assumes two seeds per cavity.

Appendix 15. Documentation Form for Non-Local Material

See Standards 11.5, 25.5, 26.1.

To be used for documenting genetic materials intended for use in *controlled parentage programs* where materials did not originate from Alberta *public land.*

Company/Agency in Possession ______________________

Submitted by ______________________

Unique Identifier ______________________

COLLECTION INFORMATION

Origin Place Name ______________________

	Original Source[1]	Plantation Collection Site[2]
Latitude	____°____'____"	____°____'____"
Longitude	____°____'____"	____°____'____"
UTM Northing	____________	____________
UTM Easting	____________	____________
Legal Location	____________	____________
Elevation	____ m	____ m

Comments ____

____

____

[1] Original location of initial wild collection to be documented where known

[2] Plantation location where material is collected from a non-wild source

GENETIC INFORMATION

Species ______________________

Male Parent Information ______________________

Female Parent Information ______________________

Comments ____

____

____

PHYSICAL INFORMATION

Type of Material ______________________

Quantity of Material ______________________

Comments ____

____

____

Note: Bold type indicates required information.

Appendix 16. Transportation or Storage of Research or CPP Parent Material Form

See Standard 12.2.

To accompany any genetic material (seed, pollen, cuttings, etc.) to be included in a *controlled parentage* or research program.
Insert one copy inside container, fasten one copy to outside of container and keep third copy for your records.

UNIQUE IDENTIFIER____________________________________
(or other identifying information, if selected before January 1, 2003)

DESTINATION FACILITY__________________________________
Mailing Address ____________________________________
____
____
Contact ________________ Phone __________ Fax __________
E-mail ______________________

COLLECTING AGENCY__________________________________
Representative__________________________________
Phone__________________________________
E-mail__________________________________

DATE OF COLLECTION __________________________________

DATE OF SHIPPING__________________________________

MATERIAL DESCRIPTION
Species__________________________________
Type of Material__________________________________
(cones, fruit, seed, pollen, cuttings, roots)
Amount of Material __________________________________
(specify measurement units: e.g. grams of seed, metres of roots, number or volume of cones)

Appendix 17. Alberta Reforestation Seed and Vegetative Materials Withdrawal and Transportation Form

See Standards 12.5.1, 12.5.3.

ALBERTA SUSTAINABLE RESOURCE DEVELOPMENT

This form is used in the tracking and inventory control of registered material. It must accompany this material during transport. A copy must be sent to the Alberta Tree Improvement and Seed Centre (ATISC), Box 750, Smoky Lake, AB T0A 3C0 or by fax (780) 656-2120.

A	B	C	D	E	F	G
REGISTERED LOT NUMBER	SUBLOT NUMBER (if applicable)	UNRESTRICTED OR RESTRICTED	TYPE OF MATERIAL	NURSERY/ PRODUCTION FACILITY	DEPLOYMENT / SEED ZONE	AMOUNT (Kg of seed or no. of vegetative)

DELIVER TO ______________________________

____

____

____

____

____

DELIVERY FROM ______________________________

____

____

____

SHIP VIA ______________________________

ORDERED BY ______________________________
(Person authorizing withdrawal)

PURPOSE ☐ NURSERY PRODUCTION
(Complete columns A, B, C, D, E, F & G)
☐ DIRECT SEEDING/PLANTING
(Complete columns A, B, C, F & G)
☐ TESTING (Complete columns A, B, & G)
☐ OTHER – Specify below.

____

____

DELIVERY DATE ______________________________

DATE ORDERED ______________________________

Appendix 18. Controlled Parentage Program Plan – Contents

See Standards 18.4.2, 24.1, 24.2.

The following topics are to be addressed in a Controlled Parentage Program Plan.

Introduction

History
- Early project development
- Cooperative structure
- Present status

Program Objectives
- Target species
  - Ecology
  - Genetics
- Needs and goals
- Improvement traits
- Similar programs in other regions

Breeding Region/Deployment Zone Delineation
- Ecological information
  - Forest types and plant communities
  - Topography
  - Parent materials
  - Climate
- Genetic information
- Administration and land use information
- Mapping

Parent Selection Plan
- Selection traits
- Selection strategy, including consideration of correlated traits (e.g. wood density and growth)
- Materials collection

Breeding/Clonal Plan

a) Seed-based programs
- First generation
  - Traits
  - Base population
  - Breeding population
  - Schedule and predicted timelines
  - Gain estimates
  - Advanced generation/*pedigree* information (where available)

b) Clonal programs
- Base population
- Traits
- Schedule and predicted timelines
- Link to breeding program, if any
- Selection intensity and target *Ne*

Genetic Field Testing Plan
- *Test* objective (e.g. *deployment zone* delineation, progeny trial)
- *Test* sites

        - Selection criteria
        - Number of *test* sites
            - *Test* site locations and descriptions
    - *Test* site protection
    - *Test* design
        - Content and structure (controls, plot structure, blocking, replication)
        - Trees per treatment per site
    - *Trial* establishment
        - Field marking
    - Site maintenance
        - Competition and ingress control
        - Maintenance of tree identification
- *Trial* measurement
    - Variables
        - Measurement schedule
        - Data management
        - Analysis

Production Plan

a) Seed-based programs

- Orchard design
    - Production design and limits (Appendix 21)
    - Design and layout
- Orchard establishment
- Orchard management
    - Pollen contamination
    - Pollen management
    - Weed, insect, and disease monitoring and control
    - Tree management
    - *Crop* management
- Permanent Sample Tree monitoring

b) Clonal programs

- *Stoolbed* design and limits (Appendix 21), or
- *In vitro* micro-propagation
    - Production design and limits (Appendix 21)
    - Design and layout
- Establishment
- Management
    - Weed, insect, and disease monitoring and control

Deployment Plan

Genetic Conservation Plan

- *In situ*
- *Ex situ*
- Considerations upon termination of tests

Link to Supportive Research Plan(s)

Reference to Additional Relevant Reports

- Genetic Test Site Information Form
- Genetic Test Establishment Report
- Genetic Test Measurement Report
- Genetic Test Analysis Report
- Parent Tree Selection Report

Appendix 19. Breeding Regions and Deployment Zones and Associated Programs as of May 1, 2002

See Standards 18.4.2, 33.6, 34.5.

Controlled parentage program seed movement guidelines and *deployment* rules differ from natural stand seed movement guidelines because seed or vegetative propagule production is carried out in *seed orchards* and *stoolbeds*.

Deployment of *seed orchard* varieties is controlled by a *breeding region/deployment zone* system. Each *breeding region/deployment zone* is based on a target *deployment* area for a single species. *Seed orchards* are mostly developed on agriculture land outside the forest zone to reduce outcrossing with contaminating pollen. Repeated collections are made from the same trees and control is exercised on genetic composition, genetic quality and genetic diversity contained in the seedlot collection. *Breeding regions* are not necessarily coincident with *seed zones*, as they are based on a target *deployment* area for a single specified species and are generally accompanied by provenance and progeny testing.

Breeding regions are initially delineated and mapped on the basis of general genetic and ecological information as well as administrative boundaries, and are reviewed and modified on the basis of further progeny and provenance testing. *Deployment zones* are delineated on the basis of prior testing for adaptiveness of the proposed genetic material in a proposed *deployment zone*.

Seed and vegetative propagule movement and *deployment* from *controlled parentage programs* and *production facilities* are unrestricted within their specific *breeding region* or *deployment zone*. However, the Department may place conditions on the use of these materials within the *breeding region* if warranted by scientific considerations. Areas within a *breeding region* or *deployment zone* boundary that are suspected to be environmentally atypical are dealt with as exclusion areas.

The *breeding region/ deployment* zoning system will be periodically updated to accommodate new projects, new scientific information, changes in tree improvement objectives or other biological considerations.

The 20 currently approved conifer *breeding regions/deployment zones* in Alberta include nine white spruce, three black spruce, five lodgepole pine, one jack pine, one Douglas-fir and one western larch (see below). It is recognized that there are other breeding programs (hardwood and softwood) under development in Alberta.

To obtain larger scale maps, contact the Land and Forest Division of the Department.

Description of Breeding Regions By Tree Species

Species	Breeding Region	Description
Lodgepole pine (Fig 3)	B1	Northern lower foothills *breeding region* dominated by mixedwood forest types. Approved operational elevations are 800 to 1200 metres.
Lodgepole pine (Fig 3)	B2	Northern upper foothills *breeding region* dominated by conifer forest types. Approved operational elevations are 1200 to 1600 metres.
Lodgepole pine (Fig 3)	C	Swan Hills area outlier foothills *breeding region* dominated by pure and mixed conifer forest types. Approved operational elevations are 800 to 1200 metres. Area of lodgepole and jack pine hybridization.
Lodgepole pine (Fig 3)	K1	Southern upper foothills breeding region dominated by conifer forest types. Approved operational elevations are 1100 to 1500 metres.
Lodgepole pine (Fig 3)	J	Clear Hills area outlier foothills breeding region dominated by mixedwood and conifer forest types, including areas of lodgepole and jack pine hybridization. Approved operational elevations are 600 to 1000 metres.
Jack pine (Fig. 3)	P1	Northeastern lowlands boreal breeding region dominated by mixedwood forest types. Approved operational elevations are 250 to 600 metres.
Western larch (Fig. 3)	M	Southern lower subalpine breeding region dominated by conifer forest types. This species is rare in Alberta. The main project objectives are conservation and restricted use for breeding region *deployment*. Approved operational elevations are 1450 to 1700 metres.
White spruce (Fig. 4)	D	Swan Hills area outlier lower foothills breeding region dominated by mixedwood forest types. Approved operational elevations are 650 to 1050 metres.
White spruce (Fig. 1)	D1	Slave Lake area boreal breeding region dominated by boreal lowland and upland mixedwood forest types. Approved operational elevations are 500 to 800 metres.
White spruce (Fig. 1)	E	Northeastern boreal lowland breeding region dominated by mixedwood forest types. Approved operational elevations are 300 to 650 metres.
White spruce (Fig. 1)	E1	Northeastern boreal lowland breeding region dominated by mixedwood forest types. Northern extension of Breeding Region E. Approved operational elevations are 250 to 600 metres.
White spruce (Fig. 1)	E2	East central sub-boreal and parkland breeding region dominated by mixedwood and parkland forest types. Project objectives include conservation and restricted *Deployment*. Approved operational elevations are 550 to 750 metres.
White spruce (Fig. 1)	G1	Northern lower foothills breeding region dominated by mixedwood forest types. Approved operational elevations are 650 to 1050 metres.
White spruce (Fig. 1)	G2	Northwestern outlier foothills breeding region dominated by mixedwood forest types. Approved operational elevations are 500 to 900 metres
White spruce (Fig. 1)	H	Northwestern boreal lowlands breeding region dominated by mixedwood forest types. Approved operational elevations are 250 to 550 metres elevation.
White spruce (Fig. 1)	I	North-central lower foothills breeding region dominated by mixedwood forest types. Approved operational elevations are 800 to 1200 in the south and 700 to 1050 metres in the north.

Description of Breeding Regions By Tree Species (cont'd)

Species	Breeding Region	Description
Interior Douglas-fir (Fig. 4)	F1	Southern montane breeding region dominated by montane mixedwood forest types. Approved operational elevations are 1300 to 1550 metres (up to 1700 m in the Porcupine Hills).
Black spruce (Fig. 2)	L1	North-central lower foothills breeding region dominated by mixedwood forest types. Approved operational elevations are 800 to 1200 metres.
Black spruce (Fig. 2)	L2	Northern lower foothills breeding region dominated by mixedwood forest types. Approved operational elevations are 800 to 1200 metres.
Black spruce (Fig. 2)	L3	Northeastern boreal lowlands breeding region dominated by mixedwood forest types. Approved operational elevations are 300 to 650 metres.

Figure 1. White Spruce Breeding Regions In Alberta

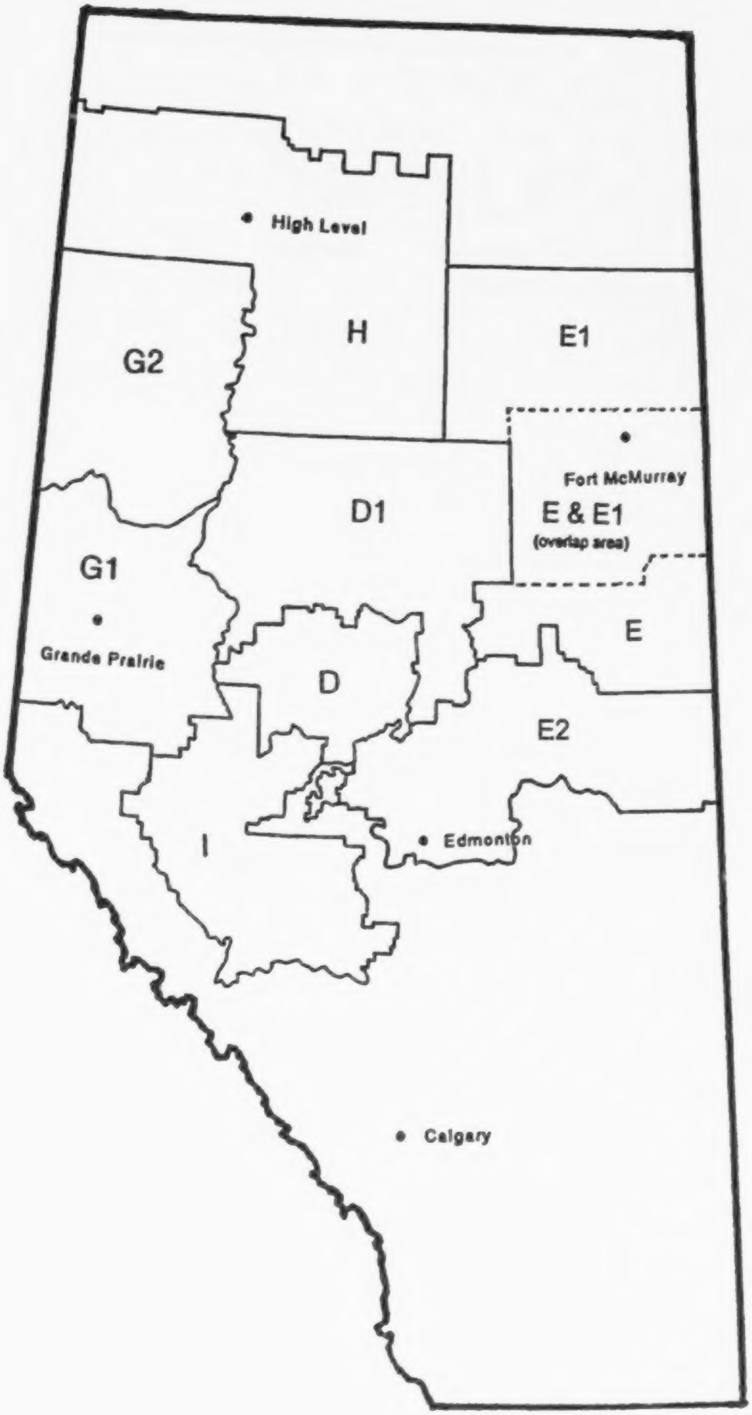

High Level
H
G2
E1
Fort McMurray
E & E1
(overlap area)
D1
G1
Grande Prairie
E
D
E2
I
Edmonton
Calgary

Figure 2. Black Spruce Breeding Regions In Alberta

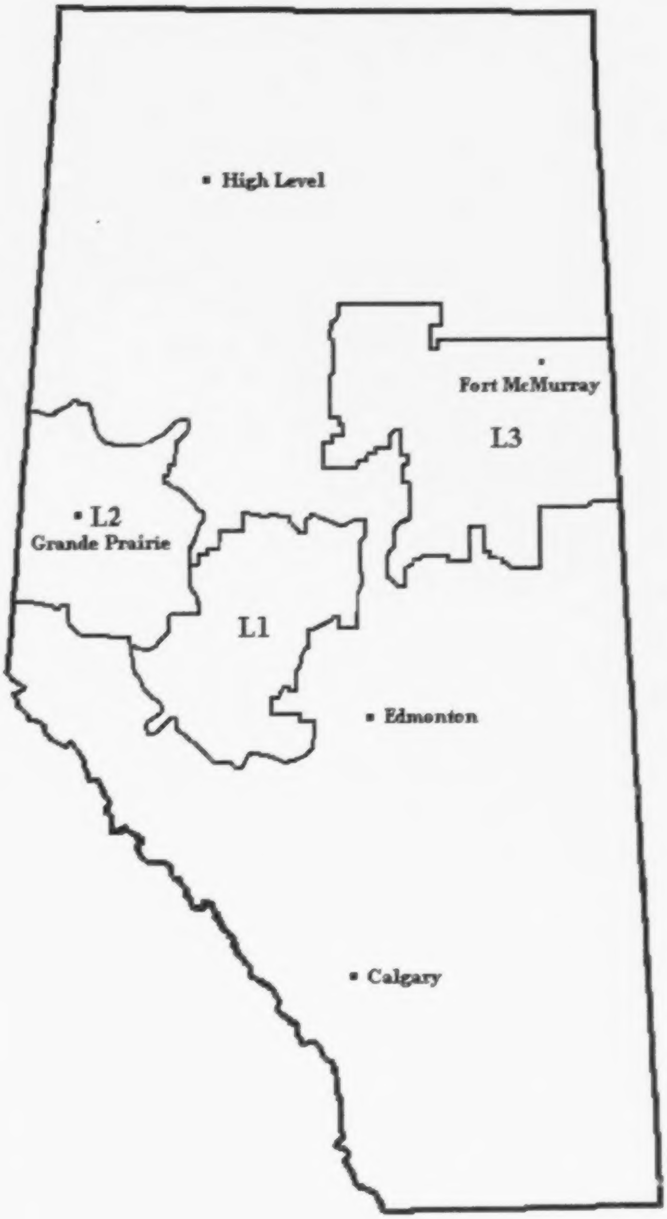

High Level
Fort McMurray
L3
L2
Grande Prairie
L1
Edmonton
Calgary

Figure 3. Lodgepole Pine, Jack Pine and Western Larch Breeding Regions in Alberta

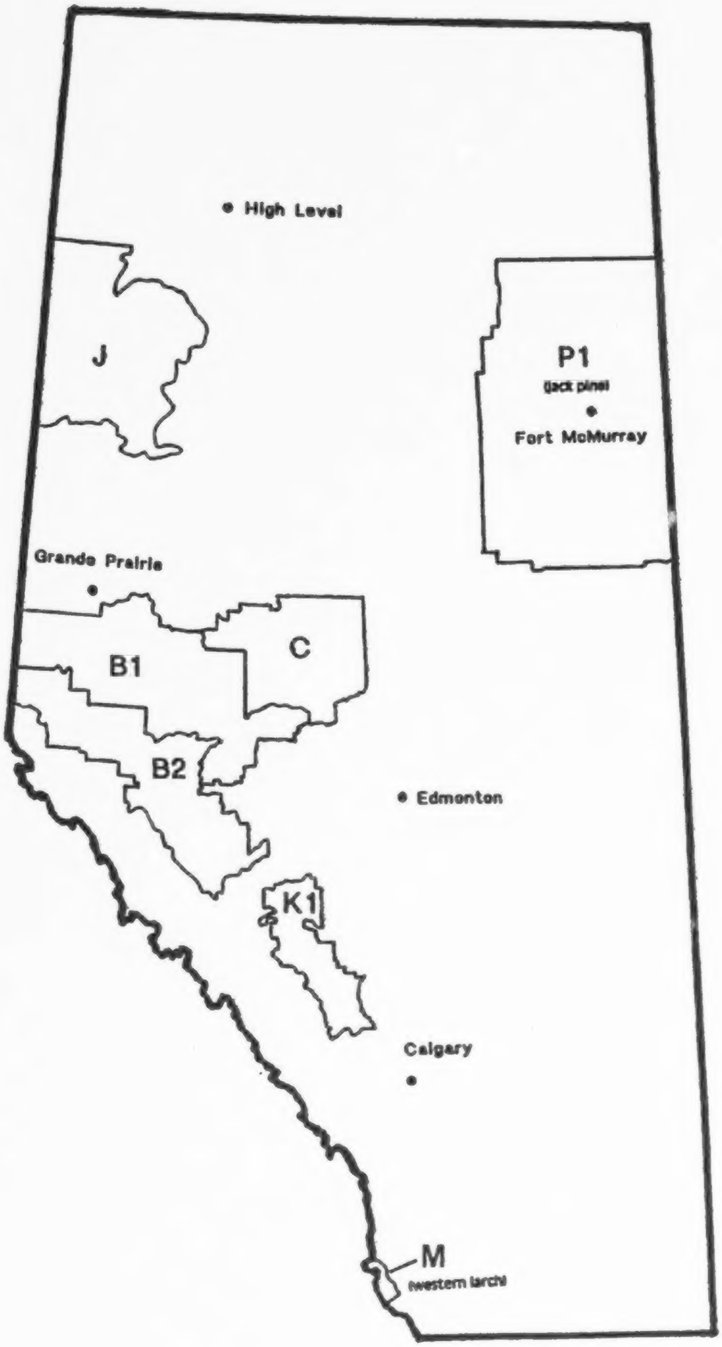
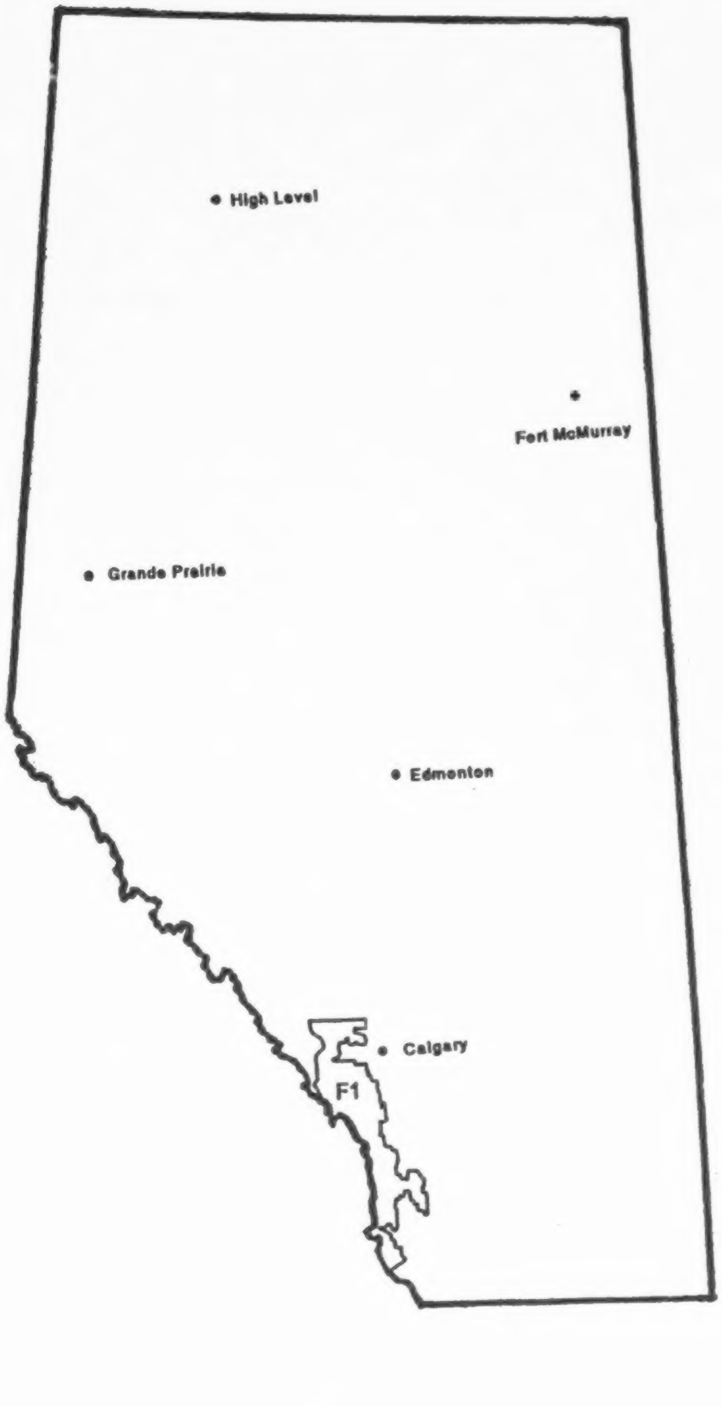

High Level
J
P1
(jack pine)
Fort McMurray
Grande Prairie
C
B1
B2
Edmonton
K1
Calgary
M
(western larch)

Figure 4. Douglas-fir Breeding Region in Alberta


High Level
Fort McMurray
Grande Prairie
Edmonton
Calgary
F1

Appendix 20. Cumulative Ne Across Production Facilities and/or Production Years

See Standards 18.4.3, 18.4.4, 32.6, 33.4.3, 33.4.4, 34.3.3.

Cumulative effective population size, or *cumulative Ne*, is the *effective population size* (Ne) of the output of a *production facility* or facilities, or of material deployed from that facility or facilities, calculated over years and/or across *production facilities*, for a given breeding region or *deployment zone*.

STEPS IN CALCULATING CUMULATIVE Ne

See below for a worked example, including three populations with subsets of 60 unrelated and non-inbred *genotypes*. Columns in Table 2 are referenced in steps.

1. For each population to be included in the cumulative assessment, calculate p_{ij}, the proportional contribution to population i by *genotype* j (example: p_{1j} p_{2j} and p_{3j} are listed in columns 2, 4 and 6 for populations 1, 2 and 3 respectively). See Appendix 36 for p_i estimation procedures.
2. Multiply the proportional contribution by the total number of plants deployed from that population (example: Table 1) to obtain n_{ij} (example: n_{1j} n_{2j} and n_{3j} are shown in columns 8, 9 and 10 for populations 1, 2 and 3 respectively).
3. Sum each *genotype*'s contribution $ntot_j$ across populations (column 11).
4. Express that number as a proportion of the total number of plants deployed (divide $ntot_i$ by the sum of column 11 entries to give pc_j values in column 12).
5. For an orchard containing unrelated and non-inbred *genotypes*, square pc_j values and sum over *genotypes* ($\Sigma\, pc_j^2$; table row 61, column 13).

And finally:

6. *Cumulative Ne* = $1/\Sigma\, pc_j^2$ (table row 62, column 13).

Note: For an orchard containing related and/or inbred *genotypes*, *cumulative Ne* would be calculated as outlined in Appendix 36, using pc_j values (e.g. column 12, rows 1-60) as the **p** vector, and generating the covariance matrix **C** (defined in Appendix 36); then *cumulative Ne* = $0.5/\mathbf{p'Cp}$.

Note that *Ne* values for each individual population are shown in columns 3, 5 and 7, row 62; the *cumulative Ne* in this example is less than the largest and greater than the smallest individual population Ne. *Cumulative Ne* will always be greater than the smallest *Ne* of individual populations, and may be larger or smaller than the largest.

EXAMPLE

Three years' production from a *seed orchard* is considered here. One bulk seedlot is collected in each of the three years. Sixty clones are included in the orchard initially; the orchard is successively rogued to 40 and then to 20 *genotypes* for years 2 and 3 respectively. *Genotypes* are non-inbred and unrelated.

Table 1. Numbers deployed from each of the three seedlots

Seedlot	Seedlot 1	Seedlot 2	Seedlot 3	Total
# deployed	600,000	850,000	200,000	1,650,000

Table 2. Genotypic contributions and calculated Ne values

	Column 1	2	3	4	5	6	7	8	9	10	11	12	13
Table row	Geno-type	p_{1j}	p_{1j}^2	p_{2j}	p_{2j}^2	p_{3j}	p_{3j}^2	n_{1j}	n_{2j}	n_{3j}	$ntot_j$	pc_j	pc_j^2
1	1	0.032	0.00102	0.098	0.00960	0.057	0.00325	19200	83300	11400	113900	0.069	0.00477
2	2	0.031	0.00096	0.035	0.00123	0.054	0.00292	18600	29750	10800	59150	0.036	0.00129
3	3	0.029	0.00084	0.015	0.00023	0.043	0.00185	17400	12750	8600	38750	0.023	0.00055
4	4	0.016	0.00026	0.042	0.00176	0.041	0.00168	9600	35700	8200	53500	0.032	0.00105
5	5	0.012	0.00014	0.023	0.00053	0.060	0.00360	7200	19550	12000	38750	0.023	0.00055
6	6	0.020	0.00040	0.022	0.00048	0.058	0.00336	12000	18700	11600	42300	0.026	0.00066
7	7	0.022	0.00048	0.006	0.00004	0.056	0.00314	13200	5100	11200	29500	0.018	0.00032
8	8	0.027	0.00073	0.047	0.00221	0.053	0.00281	16200	39950	10600	66750	0.040	0.00164
9	9	0.006	0.00004	0.031	0.00096	0.037	0.00137	3600	26350	7400	37350	0.023	0.00051
10	10	0.005	0.00003	0.004	0.00002	0.049	0.00240	3000	3400	9800	16200	0.010	0.00010
11	11	0.025	0.00063	0.016	0.00026	0.065	0.00423	15000	13600	13000	41600	0.025	0.00064
12	12	0.001	0.00000	0.030	0.00090	0.044	0.00194	600	25500	8800	34900	0.021	0.00045
13	13	0.008	0.00006	0.001	0.00000	0.042	0.00176	4800	850	8400	14050	0.009	0.00007
14	14	0.007	0.00005	0.048	0.00230	0.049	0.00240	4200	40800	9800	54800	0.033	0.00110
15	15	0.008	0.00006	0.026	0.00068	0.065	0.00423	4800	22100	13000	39900	0.024	0.00058
16	16	0.014	0.00020	0.002	0.00000	0.036	0.00130	8400	1700	7200	17300	0.010	0.00011
17	17	0.028	0.00078	0.016	0.00026	0.055	0.00303	16800	13600	11000	41400	0.025	0.00063
18	18	0.023	0.00053	0.003	0.00001	0.044	0.00194	13800	2550	8800	25150	0.015	0.00023
19	19	0.002	0.00000	0.037	0.00137	0.042	0.00176	1200	31450	8400	41050	0.025	0.00062
20	20	0.008	0.00006	0.002	0.00000	0.05	0.00250	4800	1700	10000	16500	0.010	0.00010
21	21	0.028	0.00078	0.025	0.00063	0	0.00000	16800	21250	0	38050	0.023	0.00053
22	22	0.022	0.00048	0.039	0.00152	0	0.00000	13200	33150	0	46350	0.028	0.00079
23	23	0.004	0.00002	0.035	0.00123	0	0.00000	2400	29750	0	32150	0.019	0.00038
24	24	0.027	0.00073	0.047	0.00221	0	0.00000	16200	39950	0	56150	0.034	0.00116
25	25	0.017	0.00029	0.023	0.00053	0	0.00000	10200	19550	0	29750	0.018	0.00033
26	26	0.008	0.00006	0.035	0.00123	0	0.00000	4800	29750	0	34550	0.021	0.00044
27	27	0.026	0.00068	0.006	0.00004	0	0.00000	15600	5100	0	20700	0.013	0.00016
28	28	0.004	0.00002	0.041	0.00168	0	0.00000	2400	34850	0	37250	0.023	0.00051
29	29	0.010	0.00010	0.034	0.00116	0	0.00000	6000	28900	0	34900	0.021	0.00045
30	30	0.022	0.00048	0.021	0.00044	0	0.00000	13200	17850	0	31050	0.019	0.00035
31	31	0.005	0.00003	0.002	0.00000	0	0.00000	3000	1700	0	4700	0.003	0.00001
32	32	0.032	0.00102	0.005	0.00003	0	0.00000	19200	4250	0	23450	0.014	0.00020
33	33	0.017	0.00029	0.011	0.00012	0	0.00000	10200	9350	0	19550	0.012	0.00014
34	34	0.024	0.00058	0.020	0.00040	0	0.00000	14400	17000	0	31400	0.019	0.00036
35	35	0.001	0.00000	0.005	0.00003	0	0.00000	600	4250	0	4850	0.003	0.00001
36	36	0.013	0.00017	0.021	0.00044	0	0.00000	7800	17850	0	25650	0.016	0.00024
37	37	0.006	0.00004	0.028	0.00078	0	0.00000	3600	23800	0	27400	0.017	0.00028
38	38	0.012	0.00014	0.039	0.00152	0	0.00000	7200	33150	0	40350	0.024	0.00060
39	39	0.008	0.00006	0.041	0.00168	0	0.00000	4800	34850	0	39650	0.024	0.00058
40	40	0.020	0.00040	0.018	0.00032	0	0.00000	12000	15300	0	27300	0.017	0.00027
41	41	0.006	0.00004	0	0.00000	0	0.00000	3600	0	0	3600	0.002	0.00000
42	42	0.004	0.00002	0	0.00000	0	0.00000	2400	0	0	2400	0.001	0.00000
43	43	0.009	0.00008	0	0.00000	0	0.00000	5400	0	0	5400	0.003	0.00001
44	44	0.030	0.00090	0	0.00000	0	0.00000	18000	0	0	18000	0.011	0.00012
45	45	0.030	0.00090	0	0.00000	0	0.00000	18000	0	0	18000	0.011	0.00012
46	46	0.008	0.00006	0	0.00000	0	0.00000	4800	0	0	4800	0.003	0.00001
47	47	0.018	0.00032	0	0.00000	0	0.00000	10800	0	0	10800	0.007	0.00004
48	48	0.020	0.00040	0	0.00000	0	0.00000	12000	0	0	12000	0.007	0.00005
49	49	0.010	0.00010	0	0.00000	0	0.00000	6000	0	0	6000	0.004	0.00001
50	50	0.021	0.00044	0	0.00000	0	0.00000	12600	0	0	12600	0.008	0.00006
51	51	0.030	0.00090	0	0.00000	0	0.00000	18000	0	0	18000	0.011	0.00012
52	52	0.019	0.00036	0	0.00000	0	0.00000	11400	0	0	11400	0.007	0.00005
53	53	0.010	0.00010	0	0.00000	0	0.00000	6000	0	0	6000	0.004	0.00001
54	54	0.049	0.00240	0	0.00000	0	0.00000	29400	0	0	29400	0.018	0.00032
55	55	0.030	0.00090	0	0.00000	0	0.00000	18000	0	0	18000	0.011	0.00012
56	56	0.009	0.00008	0	0.00000	0	0.00000	5400	0	0	5400	0.003	0.00001
57	57	0.015	0.00023	0	0.00000	0	0.00000	9000	0	0	9000	0.005	0.00003

	Column 1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
Table row	Geno-type	p_{1j}	p_{1j}^2	p_{2j}	p_{2j}^2	p_{3j}	p_{3j}^2	n_{1j}	n_{2j}	n_{3j}	$ntot_j$	pc_j	pc_j^2
58	58	0.011	0.00012	0	0.00000	0	0.00000	6600	0	0	6600	0.004	0.00002
59	59	0.020	0.00040	0	0.00000	0	0.00000	12000	0	0	12000	0.007	0.00005
60	60	0.021	0.00044	0	0.00000	0	0.00000	12600	0	0	12600	0.008	0.00006
61	**Sum**	1.00000	0.02284	1.00000	0.03881	1.00000	0.05145	**600000**	**850000**	**200000**	**1650000**	1.000	0.02496
62	**Ne**		**43.78**		**25.77**		**19.44**						**40.07**

where:

p_{1j} = proportional contribution of the jth *genotype* in the first population (seed or vegetative lot, or deployed population) to be included in the cumulative assessment

p_{2j} = proportional contribution of the jth *genotype* in the second population

p_{3j} = proportional contribution of the jth *genotype* in the third population

n_{1j} = total contribution of the jth *genotype* in the first population

n_{2j} = total contribution of the jth *genotype* in the second population

n_{3j} = total contribution of the jth *genotype* in the third population

$ntot_j$ = total contribution of the jth *genotype*, summed over populations

pc_j = proportional contribution of the jth *genotype*, over populations

Appendix 21. Total Production Facility Limit for Stream 2 Material

See Standards 18.4.3, 18.4.4, 24.41, 32.6, 33.4.3, 33.4.4, 34.3.3.

To maintain forest genetic diversity and associated sustainability, a limit is placed on the total number of *controlled parentage program* seedlings or vegetative propagules to be deployed from a *production facility* or facilities. This limit is applied to an entire breeding region/*deployment zone*, recognizing that there is often more than one tenure holder and/or *production facility* per region/zone.

The limit is calculated on the basis of:

- area of target strata that each tenure holder has in the region/zone,
- the number of seedlings/propagules required per hectare (Trees per ha), and
- the type of material to be produced (seedlings or vegetative propagules).

SEEDLING *production facility* limits are calculated as follows.

- Where the *Ne* is <30 (cumulative over the life of the orchard, see Appendix 20):

Planned Total Production Limit (e.g. column 6) = Area of Target Strata (e.g. column 4) x Trees per ha x 0.25

- Where the *cumulative Ne* is ≥30, these limits are doubled:

Planned Total Production Limit (e.g. column 7) = Area of Target Strata (e.g. column 4) x Trees per ha x 0.50

VEGETATIVE PROPAGULE *production facility* limits are calculated as follows.

- Where the *Ne* is <30 (cumulative over the life of the orchard, see Appendix 20):

Planned Total Production Limit = Area of Target Strata x Trees per ha x 0.20

- Where the *cumulative Ne* is ≥30, these limits are doubled:

Planned Total Production Limit = Area of Target Strata x Trees per ha x 0.40

The example below illustrates how the size of *production facilities* may be planned to meet the limits calculated as above.

Stream 2 CPP Production Facility Planning - Seedling Example

1	2	3	4	5	6	7
Participating Tenure Holder	**Total Breeding Region/ Deployment Zone Area by Tenure Holder (ha)**	**Operable Area Within Region/Zone by Tenure Holder (ha)**	**Area of Target Strata by Species and Tenure Holder * (ha)**	**Estimated Plants Required for 100% Planting of Area of Target Strata (# seedlings)**	**Planned Total Production Limit, one or more production facilities (cumulative Ne<30) (# seedlings)**	**Planned Total Production Limit, one or more production facilities (cumulative Ne≥30) (# seedlings)**
X	1,595,000	1,096,250	150,000	270,000,000	67,500,000	135,000,000
Y	957,000	817,750	87,000	156,000,000	39,000,000	78,000,000
Z	638,000	478,500	50,000	90,000,000	22,500,000	45,000,000
Totals	3,190,000	2,392,500	287,000	516,000,000	129,000,000	258,000,000

*Target strata refers to the area to be regenerated to the species produced by the *production facility*, not yield strata.

Appendix 22. Request for Deployment Variance for Stream 2 Material

See Standard 18.4.8.

DATE ____________

REQUESTING AGENCY

Agency Name ____________ Contact ____________

Mailing Address ____________

____

____

Phone ____________ Fax ____________

E-mail ____________

TYPE OF VARIANCE REQUESTED

Annual ____________ Standing ____________

Species ____________ Category of Material ____________

REASONS FOR REQUEST (Include Standards Not Met) ____________

____

____

____

____

CROP DESCRIPTION

Registered Lot Number ____________ Seed ____________ Vegetative ____________

Breeding Region/Deployment Zone ____________

Production Facility Number ____________ Effective Population Size ____________

Latitude ____________ Elevation: Mean ____________

Longitude ____________ Elevation: Range ____________

Legal Location ____________ UTM Northing ____________

UTM Easting ____________

PROPOSED DEPLOYMENT

Breeding Region/Deployment Zone ____________

Production Facility Number ____________ Effective Population Size ____________

Latitude ____________ Elevation: Mean ____________

Longitude ____________ Elevation: Range ____________

Legal Location ____________ UTM: Northing ____________

UTM: Easting ____________

Years of Deployment ____________ Total Number of Seedlings or Propagules ____________

MONITORING AND REPORTING SCHEDULE ____________

____

____

Appendix 23. Request for Planting Variance for Research Material

See Standards 23.1 and 23.7.

DATE ______________

REQUESTING AGENCY

Agency Name ______________________ Contact ______________

Mailing Address ______________________________________

____

____

Phone ______________ Fax ______________

E-mail ______________________

TYPE OF VARIANCE REQUESTED

Annual ______________ Standing ______________

Species ______________ Category of Material ______________

RESEARCH PLAN REFERENCE ______________________

MATERIAL DESCRIPTION

Origin: For progeny *tests* of local material identify *seed zone*/breeding region

____

____

Attach additional pertinent information.

PROPOSED AREA OF TESTING

Zone ______________________

Elevation ______________

Latitude ______________ Longitude ______________

Legal Location ______________________

UTM Northing ______________________

UTM Easting ______________________

Test Size (ha)______________________

BENEFIT/RISK ASSESSMENT Where *non-local materials* are involved, attach a discussion of the following topics, including relevant experience and referenced literature: a) Expected benefits; b) Estimated risks and consequences of: gene flow to native populations, invasiveness to Alberta forests, development of centres for distribution of pests and release of toxins.

MONITORING AND REPORTING SCHEDULE ______________________

____

____

____

Appendix 24. Research Program Plan – Contents

See Standard 25.1.

The following topics are to be addressed in a Research Program Plan. A proponent is advised to submit a letter of intent to the Department prior to developing a program plan.

Introduction

- Project title
- Research proponents
- Research problem
- Traits of interest
- Research objective(s)
- Hypothesis test(s)
- *Deployment* objectives where applicable
- Risk/benefit assessment where applicable[1]
- Link to *controlled parentage program*, if relevant

Materials

- Target species
- Genetic *test* material (provenances, populations, families, etc.)
- Genetic *test* material origin
- Physical *test* material (seedling, seed, rooted cuttings, stock type, etc.)
- Controls
- Physical *test* environment (e.g. lab, green house, field *test*)
- *Test* environment conditions (field *test* site location climate, soils, etc.; lab or greenhouse *test* environment conditions)

Methods

- Research hypothesis test(s)
- Experimental design
- Data collection
- Criteria for selection and protection of *test* site(s) if applicable
- Description of assessment methods and procedures
- Analysis procedures

Anticipated Deliverables
References

---

[1] e.g. Volume/growth expectations, benefit(s)
Genetic make-up (i.e. based on flowering, leaf morphology analysis, DNA analysis)
Gender
Fertility (hybridization potential [phenology, viability, control])
Suckering potential (possible control, if a *genetically modified organism* (GMO) may be specific to type)
Planting location, design, timeline, size
Buffer requirements, maintenance standards
Harvesting method and clean-up
Potential for release of toxins
Centre of insect and disease outbreaks
Potential to ameliorate risk (e.g. silviculture practices)
Invasiveness
Ecosystem impact

Appendix 25. Unique Identifier Codes

See Standard 25.5.

UNIQUE IDENTIFIER

Field Number	1	2	3	4	5	6	7	8	9	10	11	12	13
Example	D	M	0	0	0	4	5	A	W	0	0	1	S

Fields 1 - 7 provide the unique *genotype* and are compulsory fields.
Fields 8 - 13 provide the material description and are optional fields.

FIELD DESCRIPTION WITH EXAMPLE

Field Numbers	Character Type	Description	Example DM00045AW001S	Example Description
1 - 2	alpha	Agency Code	DM	Daishowa-Marubeni
3 - 7	numeric	Agency's unique clone identification number for the parent tree/selection/clone	00045	Clone number 45
8 - 9	alpha	Species Code	AW	Trembling aspen
10 - 12	numeric	Agency's identification number for the individual or collection	001	First collection
13	alpha	Type of material	S	Seed lot

Each agency's identification number for a parent tree/selection/clone (fields 3 - 7) is a unique number for that agency, and is to be used only once by that agency, regardless of the species.

All alpha fields are in uppercase letters only.

CODES

Type of Material (field 13):	*grafted ramet*	(G)
	rooted ramet	(C)
	seed lot	(S)
	scion	(N)
	root	(R)
	flower buds	(B)
	pollen	(P)
	whole tree/seedling	(T)
	other	(X)

AGENCY CODES (fields 1 - 2):

Agency Name	Code
770538 ALBERTA LTD	AA
AINSWORTH LUMBER COMPANY	AI
ALBIAN SANDS ENERGY INC	AS
ALBERTA-PACIFIC FOREST INDUSTRIES INC	AF
ALBERTA PLYWOOD LTD	AP
ALBERTA TREE IMPROVEMENT AND SEED CENTER	AT
ANC TIMBER LTD	AN
ATLAS LUMBER (ALBERTA) LTD	AL
BLUE RIDGE LUMBER	BR
BOSS TIMBER LTD	BT
BOUCHER BROTHERS LUMBER	BB
BUCHANAN LUMBER	BL
CANADIAN FOREST PRODUCTS LTD, GRANDE PRAIRIE	CG
CANADIAN FOREST PRODUCTS LTD, HINES CREEK	CH
CARDINAL RIVER COALS	CR
CYPRESS HILLS INTERPROVINCIAL PARK	CY
DAISHOWA-MARUBENI INTERNATIONAL LTD	DM
FOOTNER FOREST PRODUCTS	FF
FOREST RESOURCE IMPROVEMENT ASSOCIATION	FR
HANSEN FOREST PRODUCTS	HF
HUALLEN SEED ORCHARD COMPANY	HU
INDIAN AND NORTHERN AFFAIRS, CANADA	IN
LAND AND FOREST DIVISION, CLEARWATER AREA	LC
LAND AND FOREST DIVISION, FOOTHILLS AREA	LF
LAND AND FOREST DIVISION, LAC LA BICHE AREA	LL
LAND AND FOREST DIVISION, LESSER SLAVE AREA	LS
LAND AND FOREST DIVISION, PEACE AREA	LP
LAND AND FOREST DIVISION, SMOKY AREA	LG
LAND AND FOREST DIVISION, SOUTHERN ROCKIES AREA	LR
LAND AND FOREST DIVISION, UPPER HAY AREA	LU
LAND AND FOREST DIVISION, WATERWAYS AREA	LW
LAND AND FOREST DIVISION, WOODLANDS AREA	LO
LAND AND FOREST DIVISION, PRFN	LN
L H REHN LUMBER LTD	RE
LITTLE RED RIVER FORESTRY LTD	RR
LUSCAR LTD -COAL VALLEY MINE	CV
LUSCAR LTD –GREGG RIVER MINE	GR
LUSCAR LTD -LINE CREEK MINES	CM
LUSCAR LTD -OBED MOUNTAIN MINE	OM
MANNING DIVERSIFIED FOREST PRODUCTS	MD
MEDICINE LODGE TIMBER PRODUCTS	ML
METIS SETTLEMENTS TRANSITION COMMISSION	MS
MILLAR WESTERN FOREST PRODUCTS – BOYLE	MB
MILLAR WESTERN FOREST PRODUCTS – WHITECOURT	MW
MOSTOWICH LUMBER LTD	MO
NORTHLAND FOREST PRODUCTS LTD	NF
PEACE RIVER PULP LTD.	PR
ROCKY WOOD PRESERVERS LTD	RW
SEEHTA FOREST PRODUCTS	SF
SLAVE LAKE PULP LTD.	SA
SMOKY RIVER COALS LIMITED	SR
SOSNOWSKI, MIKE	SM

AGENCY CODES (cont'd)

Agency Name	Code
SPRAY LAKES SAWMILLS LTD	SL
ST JEAN LUMBER LTD	SJ
SUNCOR ENERGY INC	SE
SUNDANCE FOREST INDUSTRIES LTD	SU
SUNPINE FOREST PRODUCTS LTD	SP
SYNCRUDE CANADA LTD	SC
TALL PINE TIMBER COMPANY LTD	TP
TIMEU FOREST PRODUCTS	TF
TOLKO INDUSTRIES LTD – HIGH PRAIRIE	TH
TOLKO INDUSTRIES LTD – HIGH LEVEL	TL
VANDERWELL CONTRACTORS LTD	VC
WABASCA LAKES SAWMILL COMPANY LTD	WL
WALLACH, PAUL	WP
WELDWOOD OF CANADA LTD	WW
WESTERN BOREAL ASPEN CORP	WB
WEYERHAEUSER COMPANY LTD, DRAYTON VALLEY	WD
WEYERHAEUSER COMPANY LTD, EDSON	WE
WEYERHAEUSER COMPANY LTD, GRANDE CACHE	WC
WEYERHAEUSER COMPANY LTD, GRANDE PRAIRIE	WG
WEYERHAEUSER COMPANY LTD, SLAVE LAKE	WS
ZAMA MILLS	ZM

SPECIES CODES (Fields 8-9):

Section 1: Pure Species

Species Code	Family	Genus	Species	Common Name
BW	Betulaceae	Betula	*papyrifera*	paper (white) birch
PL	Pinaceae	*Pinus*	*contorta*	lodgepole pine
PJ	Pinaceae	*Pinus*	*banksiana*	jack pine
PA	Pinaceae	*Pinus*	*albicaulis*	whitebark pine
PF	Pinaceae	*Pinus*	*flexilis*	limber pine
LA	Pinaceae	*Larix*	*lyallii*	alpine larch
LT	Pinaceae	*Larix*	*laricina*	tamarack
LW	Pinaceae	*Larix*	*occidentalis*	western larch
SW	Pinaceae	*Picea*	*glauca*	white spruce
SE	Pinaceae	*Picea*	*engelmannii*	Engelmann spruce
SB	Pinaceae	*Picea*	*mariana*	black spruce
FD	Pinaceae	*Pseudotsuga*	*menziesii*	Douglas-fir
FB	Pinaceae	*Abies*	*balsamea*	balsam fir
FA	Pinaceae	*Abies*	*lasiocarpa*	alpine fir
AB	Salicaceae	*Populus*	*alba*	white poplar
PB	Salicaceae	*Populus*	*balsamifera*	balsam poplar
DA	Salicaceae	*Populus*	*davidiana*	Chinese/Korean aspen
DE	Salicaceae	*Populus*	*deltoides*	plains cottonwood
GR	Salicaceae	*Populus*	*grandidentata*	bigtooth aspen
LA	Salicaceae	*Populus*	*laurifolia*	—
MA	Salicaceae	*Populus*	*maximowiczii*	poplar (Japan)
NI	Salicaceae	*Populus*	*nigra*	poplar
SA	Salicaceae	*Populus*	*sargentii*	sargentii poplar
TA	Salicaceae	*Populus*	*tremula*	European aspen
AW	Salicaceae	*Populus*	*tremuloides*	trembling aspen
TR	Salicaceae	*Populus*	*trichocarpa*	black cottonwood

Section 2: Hybrids

Species Code	Family	Genus	Species	Common Name
Codes to be developed in the future				

Appendix 26. Genetic Test Establishment Report – Contents

See Standards 27.1 and 30.12.1.

At a minimum, the genetic *test* establishment report will contain a clear description and/or listing of the following:

Header

- Program
- Agency / cooperators
- *Trial* code
- Site name
- Reference to associated Controlled Parentage Program (CPP) or Research Plan
- List of associated *trials* (i.e. *tests* containing the same genetic material)

Test Material

- Listing of seed or vegetative lots including *genetic identity* and genetic origin

Controls

- Listing of seed or vegetative lots including *genetic identity* and genetic origin

Planting Stock

- Description and location of sowing and growing, including nursery, sowing date, lift date and stock type; also any relevant descriptive details relating to growing, lifting, packing and delivery

Experimental Design

- Type (e.g. Alpha, randomized complete block)
- Number of replicates
- Number of blocks/rep
- Plot size and shape
- Include outputs from design generation program showing treatment randomizations and replicate/block assignments
- Border row(s) description

Test Site

- Include completed Genetic Test Site Information Form (see Appendix 29) and access map

Site Protection

- Legal (e.g. DRS)
- Physical (e.g. fencing)

Site Preparation

- Method
- Timing
- Contractor

Site Layout

- Method
- Spacing

Field Marking

- Description
- % trees marked

Planting

- Names of contractors and key supervisors
- Dates
- Weather
- Planter allocation description (e.g. one planter/rep)

Map or Maps

- Must unambiguously define genetic and experimental design identity of each tree

Test Content File

- Attach electronic listing as per Standard 27.1

References

Appendix 27. Genetic Test Measurement Report – Contents

See Standards 27.4, 30.8.1, 30.12.2.

At a minimum, the genetic test measurement report will contain a clear description and/or listing of the following.

Introduction
- *Trial* description and objective(s)
- Applicable CPP or RP Plan
- Measurement objectives
- Measurement schedule
- Measuring agency and personnel

Methods
- Variables assessed and measured
- Assessment and measurement methods, procedures and equipment
- Quality control procedures (e.g. measurement procedures, data handling and verification procedures, field measurement spot checking and sampling intensity, measurement instrument calibration)

Results
- Data dictionary containing variable listing, description of values of variables, position in file and file format
- Data format (ASCII standard)
- Measurement start and completion dates
- Data summaries
  - Tree counts by site, replicate and treatment
  - Appropriate site means and ranges for assessed traits
  - Trait means by replicate
  - Trait means by treatment
- Attach verified raw data set to be submitted electronically with report and in accordance with data handling standards outlined in Standard 27.0.

Notes
- Significant items of interest or concern relating to assessment or data

Appendix 28. Genetic Test Analysis Report – Contents

See Standard 30.1.

At a minimum, the genetic test analysis report will contain a clear description and/or listing of the following.

Name of Relevant CPP or RP Plan

Genetic Test Analysis Report

- *Trial* identity
- Filename of validated dataset (submitted with Genetic Test Measurement Report; see Appendix 27 for contents)
- Objective(s) of analyses
- Editing procedure used to convert validated dataset to dataset analyzed (e.g. treatment of outliers, values deleted, reasoning)
- Analytical procedure
    - Method (e.g. ANOVA, BLP)
    - Model
    - Expected mean squares where appropriate

Summary Statistics for Traits of Interest (e.g. height and survival)

Estimates of Genetic Parameters (e.g. *breeding values*, heritability and genetic correlations)

- Showing method and formulae used

Standard Errors

- Calculated for parameter estimates used to calculate heritability and genetic correlations
- Calculation methods to be shown

Dataset Analyzed

- Submitted in electronic format with this analysis report

Appendix 29. Genetic Test Site Information Form

See Standard 30.3.2.

Relevant CPP or RP Plan		
Proponent responsible for test site		
Date form completed/updated		
Trial code (provided by the Department)		
Site name (local feature or landmark)		
Land reservation (type: e.g. ISP or MLL, date, identification number)		
Site location	Latitude	
	Longitude	
	Legal	
	UTM Northing (optional)	
	UTM Easting (optional)	
Site information	Elevation (m)	
	Slope (range and mean)	
	Position on slope	
	Aspect	
	Opening size	
	Parent material	
	Soil classification	
	Natural region	
	Natural subregion	
	Original species composition and cover type	
	Site classification/ type	
	Productivity	
	Effective rooting depth	
	Soil type and depth	
	Drainage class	
	Nutrient class	
	Other soil information	
Site history	Harvest date	
	Post harvest (site prep) treatment, date(s)	
	Other development info (fence, culvert, etc.)	
Maps (attach)	Site access (sketch ok)	
	Site (cutblock) map to scale	

Appendix 30. Example of Data Collection Map and Corresponding Form

See Standard 30.5.1.

EXAMPLE OF DATA COLLECTION FORM (Excel Sheet)

This form may be used as a template for any trial. Therefore, not all columns will be relevant to all trials. For silvicultural trials there will be a treatment column; for genetics trials there may be a provenance and clone column. Although the site code must exist in the file, the column can be hidden when printing out the sheets for data entry purposes. Each year that the file is added to will require the insertion of a new column for the trait being measured. For example: FHt99|FHt00|FHt01|FCp99|FCp00|FCp01|, etc. It is very useful to print out at least the last year's measurements when preparing data sheets, while hiding all other information. This can also be done if data is being collected directly onto a computer.

(FHt99: Fall Height 1999)

Page:__ of __

Location ____________________

Trial Code ____________________

Year of Planting____________________

Measurement Date ____________________

Recorders' Names ____________________

Contractor ____________________

Excel line	Site Code	Replicate	Clone or Family	Tree	Height (cm or m) Indicate fall /spring and the year (e.g. FHt99)	RCD (cm) or DBH (cm) Indicate fall /spring and the year (e.g. FCp99)	Survival 0=dead 1=alive	COMMENTS
9		1	100	1				
10		1	100	2				
11		1	405	1				
12		1	405	2				
etc								

TREE FORM 4 Page 1 of 2

EXAMPLE OF MAP GUIDE FOR TRIAL INSTALLATIONS

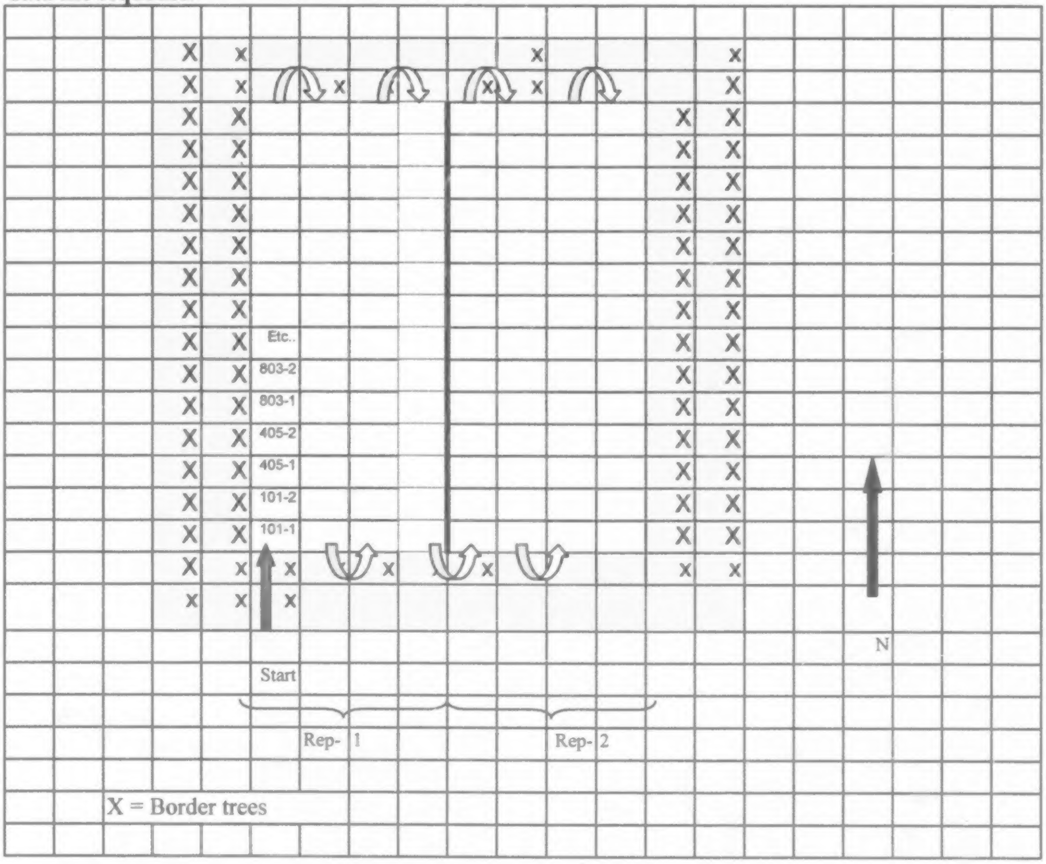
MAP GUIDE

Page__ of __

Location____________________________
Plantation name or trial code_________________
Measurement date____________________ Year of planting______________
Contractor___________________________ Initials of recorders____________________

On the grid indicate the tie point, direction of travel throughout plantation/trial.
Show North arrow
Include replicate, clone or treatment and tree number per grid square.

Clearly indicate Start point of map to link with data file sequence.



Include as many grids as needed to cover plantation/trial and include tie points between maps.
Indicate border trees with shading or X's.
Comments:

MAP GRID

Appendix 31. Calculation of Genetic Worth for Vegetative Lots and Orchard Seedlots

See Standards 31.2, 33.3, 33.6, 34.1, 34.5. See also Appendix 28.

INTRODUCTION

Genetic worth (GW) is an estimate of the expected performance of a vegetative or seed lot, and refers to individual traits such as height, volume or wood density. It is calculated as the average *breeding value* (BV) of *genotypes* represented in the lot, weighted by genotypic contribution (for vegetative lots), or by an estimate of the proportion of gametes contributed by each *genotype* (for seedlots). The *genetic worth* of orchard seedlots may need to be adjusted for genetic (pollen) contamination and supplemental mass pollination (SMP).

APPLICABILITY

Where application or claim for *genetic gain* is contingent on the *genetic worth* of a seedlot or seedlots used for *reforestation*, *genetic worth* shall be calculated according to the protocols outlined here. Where no claim for *genetic gain* applies, *genetic worth*, for the purpose of lot *registration*, can be considered to be 0.

ASSUMPTIONS AND CALCULATIONS

1. It is assumed that phenotypic selection from *wild* stands will yield, on average, a 2% gain in height, where selections have been made intensively and there is documented height over age superiority. This figure may be used as a BV for selected clones until reliable *test* results are available (see Table 1, Standard 31.5). Individuals in seedling *seed orchards* will be assigned a BV of 1% until reliable *test* results are available.

2. BVs for height, estimated from genetic *test* data, are calculated relative to unselected or operational lot controls appropriate to the given *controlled parentage program* (CPP), or to the mean performance of progeny of parents in the *breeding population* of the CPP. Where BVs are calculated relative to the mean of tested parents (rather than relative to control lots), and selections were made intensively as described in Item 1 above, 2% may be added to the calculated BV.

3. The genetic correlation between height at rotation age and height at assessment age is based on Lambeth's (1980) model, and may be calculated as:

$$\mathbf{r_a(j,m) = 1.02 + 0.308Ln(j/m)}$$

where

$r_a(j,m)$ = the additive genetic correlation between performance at ages j and m, assessment (juvenile) and rotation (mature) ages respectively; and

$Ln(j/m)$ = the natural logarithm of the age ratio j/m.

4. It will be assumed that the *genetic worth* of contaminating pollen is 0, unless evidence to the contrary exists.

5. p_i, the proportion of gametes produced by *genotype* i, will be estimated as follows.

A. Seed lots from clonal and/or uneven-aged seed orchards

Method of estimation will depend on the number of *genotypes* contributing to the *crop*. See Table 1. Where genotypic frequencies are calculated based on both male and female contributions, male and female genotypic contributions may be calculated separately. Otherwise, male and female contributions for *genotype* i are both assumed to equal p_i.

Table 1. Method of genotypic contribution estimation for clonal and/or uneven aged orchards

Number of genotypes contributing	Method of estimation of genotypic contribution
Fewer than 50	As per Table 1, Appendix 37. Alternatively, if collections are made on a clonal basis, cone volume per clone may be used to estimate p_i.
50 – 74	Sampling level: 50% sample of contributing trees Material assessed: count of female flowers or cones Alternatively, if collections are made on a clonal basis, cone volume per clone may be used to estimate p_i.
75 or more	Genotypic frequency in the cone-bearing population may be used to estimate p_i. Example: Clone x has 15 *ramets* that bear cones out of an orchard total of 250 cone-bearing *ramets*. $p_i = 15/250 = 0.06$. Alternatively, if collections are made on a clonal basis, cone volume per clone may be used to estimate p_i.

B. Seed lots from even-aged half-sibling family orchards

Method of estimation will depend on number of families contributing to the *crop*. See Table 2. Where genotypic frequencies are calculated based on both male and female contributions, male and female genotypic contributions may be calculated separately. Otherwise, male and female contributions for family i are both assumed to equal p_i.

Table 2. Method of genotypic contribution estimation for even-aged half-sibling family orchards

Number of families contributing	Method of estimation of genotypic contribution
Fewer than 25	As per Table 1, Appendix 37. Alternatively, if collections are made on a family basis, cone volume per family may be used to estimate p_i.
25 – 37	Sampling level: 50% sample of contributing trees Material assessed: count of female flowers or cones. Alternatively, if collections are made on a family basis, cone volume per family may be used to estimate p_i.
38 or more	p_i = proportion of orchard trees of family i

C. Vegetative lots

p_i = proportion of vegetative propagules produced by *genotype* i

SEVERAL CASES ARE CONSIDERED BELOW.

CASE 1. Seed or vegetative lot produced in production facility with no genetic contamination or supplemental mass pollination (SMP)

$$GW = \sum(p_i BV_i)$$

where

GW = *genetic worth* of the seed or vegetative lot;

BV_i = *breeding value* of *genotype* (clone or family) i

Example 1: Breeding values and genotypic contributions as shown in table below.

Genotype	p_i	BV_i	p_i*BV_i
1	0.10	0.27	0.027
2	0.07	0.20	0.014
3	0.05	0.15	0.0075
4	0.09	0.22	0.0198
5	0.14	0.06	0.0084
6	0.07	0.10	0.007
7	0.05	0.08	0.004
8	0.04	0.12	0.0048
9	0.03	0.02	0.0006
10	0.11	0.02	0.0022
11	0.07	0.02	0.0014
12	0.06	0.02	0.0012
13	0.05	0.02	0.001
14	0.07	0.02	0.0014
Sum	**1.00**		**0.10**

Thus for this lot

GW = 0.10, or 10%

CASE 2. Seedlot produced in production facility where pollen contamination exists

$$GW = 0.5\sum[(1-PC)*BVM + PC*BVC + BV_i]* p_i$$

where

PC = proportion of contaminating pollen (see Appendix 34 for calculation methods)

BVM = average male BV, weighted by genotypic contributions

BVC = BV of contaminant pollen

[other variables as above]

If the contaminant pollen has a BV of 0, this simplifies to

$$\begin{aligned} GW &= 0.5\sum\{(1-PC)*BVM + BV_i\}* p_i \\ &= 0.5[(1-PC)*BVM + \sum(BV_i)* p_i] \end{aligned}$$

Example 2: Breeding values and genotypic contributions as in Table 1.

$PC = 0.23$

BVC is assumed to be 0.

Thus

$$\begin{aligned} GW &= 0.5*[(1-0.23)*0.1003 + 0.1003] \\ &= 0.5*[.0772 + .1003] \\ &= 0.09\text{, or } 9\% \end{aligned}$$

CASE 3. Seedlot produced in production facility with pollen contamination and supplemental mass pollination (SMP)

$$GW = 0.5\sum[PSMP_i*BVSMP_i + (1-PSMP_i)\ [(1-PC)*BVM + PC*BVC] + BV_i]* p_i$$

where

$PSMP_i$ = proportion of successful SMP applied to clone i

$BVSMP_i$ = average BV of successful SMP applied to clone i

[other variables as above]

REFERENCES

Lambeth, C.C. 1980. Juvenile-mature correlations in Pinaceae and implications for early selection. For. Sci. 26: 571:580.

Woods, J.H., M.U. Stoehr and J.W. Webber. 1996. Protocols for rating seed orchard seedlots in British Columbia. BC Ministry of Forests, 26 p.

Xie, C.-Y. and A.D. Yanchuk. [accepted 2002]. Breeding values of parental trees, genetic worth of seed orchard seedlots and yields of improved stocks in British Columbia. Accepted for publication in W.J.A.F.

Appendix 32. Production Facility Establishment Report and Updates

See Standard 32.8.1.

Establishment reports are due February 28 in the year following the establishment of the production facility. Establishment reports for seed facilities must contain the following information (for details, refer to sample establishment report on the Department's website). For vegetative production facilities, complete as appropriate. Contact the Department for information

Project Title

Location
- Site name
- Legal land description
- Latitude and longitude
- Elevation

Site Information
- Physical description
- History of site use

Parent Material Description
- List of material comprising the orchard population

Orchard Stock
- Description of rearing regime
- Rootstock provenance

Orchard Design
- Design software used
- Constraints on spacing of related clones

Planting Report
- Planting date
- Planters' names
- Weather conditions

Origin of Clones Table
- Clone or family number
- Collection site
- Latitude and longitude
- Elevation

Distribution of Clones
- Listing of *ramets* per clone planted in the orchard keyed to planting year
- *Ramets* per clone in the clone bank
- Inventory of potted grafts per clone

Planting Plan
- List of grafts planted in the current year including clone and *ramet* number and planting position in the orchard

Orchard Layout Map

- Showing all orchard positions with planted positions keyed to year of planting

Site Layout Map

- Showing position of orchard in relation to other plantations on site

Access Map

- Providing directions to the orchard

As changes occur (e.g. mortality, replacement, roguing), the above items should be updated and submitted to the Department.

Appendix 33. Permanent Sample Tree (PST) Protocols

See Standard 32.8.2.

PST System for Flowering and Seed Production Monitoring in Alberta Seed Orchards

PURPOSE

- To provide orchard-specific local data for monitoring *seed orchard* development, flowering, cone and seed production, and seed quality, and
- To provide an estimate of reproductive contribution and a tool for cone *crop* forecasting.

SAMPLE SIZE

- For orchards with an intended maximum of up to 600 *ramets* (trees), the final number of PSTs designated is 60.
- For orchards with an intended range of 600-2000 *ramets* (trees), the final number of PSTs designated is 10% of intended number of *ramets* (trees).
- For orchards with an intended maximum greater than 2000 *ramets* (trees), the final number of PSTs designated is 200.
- In the case of clonal orchards, PSTs are added annually to proportionately represent each planting year.
- In clonal orchards, an attempt should be made to sample all clones represented by five or more *ramets*.
- PSTs should be well distributed across the orchard.

DATA COLLECTED

- Height to the nearest cm to tip of terminal bud
- Crown width at widest part of crown through one plane to nearest cm
- DBH (diameter at breast height) to nearest cm, once grafts are at least 10 years old
- Number of male and female flowers: actual count or actual estimate if flowering is prolific (For actual estimate, count flowers on one representative branch, count number of flower bearing branches and multiply.)
- Cone production (in the case of pine species, both mature and immature cones)
- Stacked cone volume (cones per litre)
- Seed yield (seeds per cone)
- 1000 seed weight
- Seed germination %
- Insect and disease assessment

Note: Cone counts are completed for each individual PST. Cones are then bulked into a separate PST collection for insect/disease assessment, seed yield calculations and germination testing. Cone and seed processing of the PST collection are done independently of the operational collection.

ASSESSMENT SCHEDULE

Assessments are completed annually except for growth trait measurements, i.e. height, crown width and DBH. These are done annually until the orchard is fully established and then measurements are completed every second year.

DATA SUMMARIES

Data are added annually to an electronic database maintained for each orchard. Data are to be summarized and reported in the Annual Operations Report (Appendix 35) as illustrated in the following template tables.

Table 1. Template: PST Summary of seed production and monitoring information

Summary of Seed Production and Monitoring Information for Region X Seed Orchard

Line	**Orchard Characteristics**	**Result**
1.	Orchard design capacity	
2.	Total no. of seed trees established	
3.	Total no. of clones/families established	
4.	Average age	
5.	Age range	
6.	Average height (cm ± SE)	
7.	Height range	
8.	Average crown width (cm ± SE)	
9.	Crown width range	
10.	Total no. of PSTs	

Reproductive Balance

11.	No. of PSTs flowering	
	Male Flowering	
12.	No. of PSTs with male flowers	
13.	Mean no. of male flowers/PST	
14.	Standard error of (line 13)	
15.	Range of male flowers/PST	
	Female Flowering	
16.	No.of PSTs with female flowers	
17.	Mean no. of female flowers/PST	
18.	Standard error of (line 17)	
19.	Range female flowers/PST	
20.	Mean male-female flower production ratio	

Line	**Immature Cone Production**	**Result**
21.	Date assessed	
22.	No. of PSTs producing cones	
23.	Mean no. of cones/PST	
24.	Standard error of (line 23)	
25.	Range of cones/PST	
26.	**Cone crop estimate (# of cones)***	
27.	**Cone crop estimate (hectolitres)****	

Cone Production

28.	No. of PSTs producing cones	
29.	Mean no. of cones/PST	
30.	Range of cones/PST	
31.	Total no. of cones from all PSTs	
32.	Mean no. of cones/litre	

Seed Production

33.	Seed production (g)	
34.	No. of seeds/cone	
35.	1000 seed weight	
36.	Germination %	

*** For all species except pine (line 2) x (line 17)**

*** For pine species (line 2) x (line 23)**

**** To estimate hectolitres divide (line 26) by the appropriate factor:**

For white spruce – 15,000 cones/hl
For black spruce – 24,000 cones/hl
For lodgepole pine – 3,800 cones/hl

Table 2. Template: Annual summary of PST data

Annual Mean Summary of PST Data for Region __ Seed Orchard

Year	Height (cm)	Crown Width (cm)	Male Flowers	Female Flowers	Immature Cones	Mature Cones

Appendix 34. Pollen Contamination and Phenology Monitoring

See Standard 32.8.3.

Note: These are interim guidelines only. A comprehensive reassessment of monitoring requirements should be undertaken when data have been collected.

PART 1. POLLEN CONTAMINATION ESTIMATION

Pollen contamination can reduce the genetic worth of a seedlot or in extreme cases render a seedlot maladapted. Pollen monitoring will be used to estimate contamination levels.

GUIDELINES

- The orchard manager will monitor pollen flight within each orchard at a minimum of two locations, and preferably four.
- The orchard manager will monitor pollen flight outside the orchard at a minimum of two regional monitors for each orchard complex. Regional monitors may be established within orchards that have not yet begun to produce pollen.
- Regional monitors should ideally be located in an open area, a minimum of 300 m from the orchard boundary and not downwind from the orchard.
- The type of pollen monitoring device used is the responsibility of the orchard manager but the manager must ensure that daily pollen cloud density values can be reliably generated.
- Traps should be changed at least every two days, and every day during periods of peak flight.
- Pollen counts will be expressed as grains per square mm over the change interval (generally 24 hours to 48 hours), averaged over directions if directional monitors are used, and summed over the monitoring period. Total counts will then be averaged over all monitors of each category (regional or within-orchard).
- All traps should be erected and counts begun at least two weeks before pollen flight in the orchard is expected to begin, and should be continued for several days after pollen counts of target and surrogate species have dropped to 0, both within and outside the orchard.
- For pine orchards, within-orchard monitors should be located at a height of one-half of the average crown height of the orchard.
- For spruce orchards, within-orchard monitors should be located at a height of three-quarters of the average crown height of the orchard.

OTHER CONSIDERATIONS

Pollen differentiation by visual means is virtually impossible within genera. Thus white spruce pollen cannot be distinguished from black spruce pollen, nor lodgepole pine from jack pine, or aspen from balsam poplar. In the future, molecular techniques may enable direct and more accurate assessment of pollen contamination levels.

ESTIMATION OF CONTAMINATION LEVELS

Since it is impossible to differentiate visually between pollen produced within an orchard and pollen of the same species originating outside the orchard, the amount of foreign pollen cannot be estimated directly. Instead, a surrogate species or genus with recognizably distinct pollen can be used to provide an estimate of the proportion of outside pollen that penetrates into an orchard (e.g. for a pine orchard, tamarack or spruce can be used as a surrogate).

The external (outside-orchard) pollen levels of the surrogate species and target species (**xs** and **xt**, respectively) are estimated by the orchard manager using regional monitors. The within-orchard pollen levels of the surrogate and target species (**ws** and **wt**, respectively) are measured using orchard monitors.

The ratio of pollen density within the orchard to pollen density outside the orchard, in the open, can then be calculated for the surrogate species. This ratio is assumed to be independent of time, so that the surrogate need not be flowering simultaneously with the target species. It is assumed that the proportion of target species pollen penetrating the orchard from outside will be the same as the proportion of surrogate species pollen penetrating from outside. Thus this ratio also reflects the ratio of within-orchard to outside-orchard levels of non-orchard or contaminating, target species pollen. This ratio is expected to be considerably less than 1 for a mature orchard, due to altered wind speed and patterns, and the screening effect of the orchard trees.

Thus the contaminant pollen level for the target species, **ct**, within the orchard can be estimated as

$$\mathbf{ct} = \mathbf{ws/xs\ (xt)}$$

and the proportion of contaminant pollen, **pc**, within the orchard can be estimated as

$$\begin{aligned}\mathbf{pc} &= \mathbf{ct/wt} \\ &= \mathbf{(ws*xt)/(xs*wt)}\end{aligned}$$

where

ct = contaminant pollen level of target species
ws = within-orchard pollen level of surrogate species
xs = outside orchard pollen level of surrogate species
xt = outside orchard pollen level of target species
wt = within-orchard pollen level of target species
pc = proportion of contaminant pollen (within-orchard target species pollen that originated outside the orchard)

This number, **pc**, is used in the calculation of *genetic worth* of orchard seedlots (see Appendix 31).

EXAMPLE
A pine orchard has been established in an area where spruce pollen is present in significant amounts; thus spruce can be used as the surrogate species. There are two regional monitors, R1 and R2, and three within-orchard monitors, O1 – O3. Counts for both species are shown in the table below. They were taken from directional monitors and averaged over directions.

Pollen counts (grains/mm^2) from orchard pollen monitors, averaged over directions

Date	Spruce R1	Spruce R2	Spruce O1	Spruce O2	Spruce O3	Pine R1	Pine R2	Pine O1	Pine O2	Pine O3
02.05.15	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
02.05.17	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
02.05.19	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
02.05.21	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
02.05.23	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
02.05.24	0.7	0.8	0.3	0.4	0.3	0.0	0.0	0.0	0.0	0.0
02.05.25	1.4	1.6	0.7	0.8	0.6	0.0	5.9	0.0	0.4	13.7
02.05.26	0.8	0.8	0.3	0.4	0.3	4.5	5.0	12.6	12.0	11.4
02.05.27	0.2	0.2	0.0	0.2	0.0	9.2	10.2	25.9	24.7	23.4
02.05.28	0.0	0.0	0.2	0.0	0.1	4.8	5.3	13.5	12.9	12.3
02.05.29	1.6	1.7	0.7	0.9	0.7	0.8	0.9	2.2	2.1	2.0
02.05.30	1.5	1.6	0.7	0.8	0.6	0.0	0.0	0.0	0.0	0.0
02.05.31	2.3	2.6	1.1	1.3	1.0	10.1	11.1	28.3	20.0	25.6
02.06.01	0.4	0.5	0.2	0.2	0.2	9.4	10.3	26.2	24.9	23.7
02.06.02	0.8	0.9	0.4	0.5	0.3	15.1	16.6	42.1	40.1	38.1

Pollen Counts (cont'd)

Date	Spruce R1	Spruce R2	Spruce O1	Spruce O2	Spruce O3	Pine R1	Pine R2	Pine O1	Pine O2	Pine O3
02.06.03	2.9	3.2	1.3	1.6	1.2	2.7	3.0	7.5	7.2	7.2
02.06.04	7.3	8.0	3.4	4.0	3.0	5.4	5.9	15.1	14.3	13.6
02.06.05	5.4	6.0	2.5	3.0	2.3	18.8	20.7	52.7	50.2	47.7
02.06.06	3.0	3.3	1.4	1.7	1.2	67.1	51.8	101.0	95.8	119.3
02.06.07	1.1	1.2	0.5	0.6	0.4	34.9	38.4	97.8	93.2	88.5
02.06.08	0.0	0.0	0.0	0.0	0.0	19.2	21.2	53.9	51.3	48.7
02.06.10	1.0	1.1	0.4	0.5	0.4	6.8	7.4	19.0	18.1	17.2
02.06.12	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.0	0.0
02.06.14	0.0	0.0	0.0	0.0	0.0	6.2	6.9	17.5	16.6	15.8
02.06.16	0.0	0.0	0.0	0.0	0.0	0.9	0.9	1.9	2.3	2.2
02.06.18	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
02.06.20	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
02.06.22	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
02.06.24	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Sum	**30.5**	**33.5**	**14.1**	**16.9**	**12.6**	**215.9**	**221.3**	**517.1**	**486.1**	**510.3**

xs = (30.5+33.5)/2 = 32.0
ws = (14.1+16.9+12.6)/3 = 14.6
xt = (215.9+221.3)/2 = 218.6
wt = (517.1+486.1+510.9)/3 = 504.5

Thus the pollen contamination for this pine orchard in 2002 is estimated at

pc = (ws*xt)/(xs*wt) = 0.20

Part 2. Phenology monitoring

Phenology monitoring allows the orchard manager to identify clones that are receptive either later or earlier than the bulk of the orchard population. Together with pollen monitoring, it also allows the manager to relate patterns of within-orchard pollen flight to periods of orchard receptivity, and to identify clones that may not be successfully pollinated.

It is believed that periods of pollen flight of local and contaminating pollen are coincident in Alberta *seed orchards*. Monitoring the phenology of orchard trees and relating it to pollen flow within and outside the orchard will provide an empirical *test* of this assumption.

SAMPLING LEVEL

Permanent Sample Trees (PSTs) may be used for phenology monitoring. At least one *ramet* of each clone represented in the PST population will be monitored from approximately stage 3 (see below) until stage 7, at intervals of two days or less.

White spruce female bud and reproductive phenology

Stage	Female Bud Description
1	dormant bud – bud scales dry; no swelling
2	early bud swell – pointed tip, scales shiny, resinous, dark brown
3	late bud swell – bud elongates, becomes oblong; identifiable
4	early flushing – ovuliferous scales (o.s.) visible through bud scales; bud scales partially rip off
5	advanced flushing – cone becoming erect, some o.s. at central portion separate
6	fully receptive – cone erect, o.s. separate and bend perpendicular to cone axis
7	post-receptive – cone scales closing

Lodgepole pine female reproductive phenology

Stage	Female Bud Description
1	seed cone still fully contained within shoot bud scales
2	seed cone bud still contained within flower bud scales
3	seed cone starting to emerge; rosette of cone scales just visible; not receptive
4	seed cone emerging; some pollen may reach ovules;
5	advanced flushing seed cone emerged but not fully open; cone axis not elongated; pollen may reach ovules
6	fully receptive - seed cone emerged and spaces between scales allow pollen to sift down to the ovules
7	post-receptive- cone scales thickened, preventing pollen entry

- A clone is considered receptive when 20% of the cones are fully receptive (stage 6).
- A clone is considered to have completed receptivity when 80% of the cones are post-receptive (stage 7).
- The orchard is considered receptive when 20% of clones are receptive, and to have completed receptivity when 80% of clones are unreceptive.

REFERENCES

Owens, J.N. 1984. The reproductive cycle of lodgepole pine. BC Ministry of Forests. 29p.

Owens, J.N. and M. Molder. 1984. The reproductive cycle of interior spruce. BC Ministry of Forests. 31p.

Appendix 35. Production Facility Annual Operations Report

See Standard 32.8.4.

Annual operations reports are due February 28 in the year following the year in which the operations took place. Annual operations reports for seed facilities must contain the following information (for details, refer to the sample report located on the Department's website. For vegetative production facilities, complete as appropriate. Contact the Department for information

Name of the Relevant CPP Plan

Orchard Description

- Name, number, location
- Manager
- Area occupied (ha)
- Design capacity (# clones, parents, trees)
- Number of grafts established

Cultural Activities

- Irrigation
- Fertilization
- Vegetation management (mowing, herbicide applications, etc.)
- Crown management (topping, lower branch pruning)
- Flower induction
- Supplemental pollination

Insect and Disease Incidence

- Monitoring methods
- Control measures

Other Activities

- Activities that may not occur annually but have an impact on orchard composition, e.g. roguing, thinning

Orchard Monitoring

- PST report (see Appendix 33)
- Pollen density and phenology of orchard receptivity (see Appendix 34)

Cone and Seed Production

- Timing and method of cone collection
- Total cone production (hectoliters)
- Total seed production (grams)
- 1000 seed weight
- Germination %
- *Effective population size* (see Appendix 36)

Subsequent Years' Planning

- Report on items that may affect *registration* of *crops* or licensing of facilities

Appendix 36. Calculation of Effective Population Size (Ne) for Vegetative Lots and Orchard Seedlots

See Standards 33.4, 33.6, 34.3, 34.3.1, 34.5.

INTRODUCTION

Calculation methods presented here for *effective population size* of seed or vegetative lots produced by unrelated, non-inbred *genotypes* are based on the work of Robertson (1961) and developed in Kang and Namkoong (1988); formulae developed elsewhere may give very different results.

Calculation methods for *effective population size* of seed or vegetative lots produced by orchards or *stoolbeds* containing inbred or related *genotypes*, such as half-sib seedling orchards, involve coancestry values, and are based on the work of Lindgren and Mullin (1998), who generalized earlier work.

FORMULAE

Effective population size of a seed or vegetative lot can be calculated as

$$Ne = 0.5/(\Sigma\Sigma\, p_i\, p_j\, c_{ij}) \quad (i, j = 1, 2, \ldots, n) \qquad (1)$$

or, in matrix notation

$$Ne = 0.5/\mathbf{p'Cp} \qquad (2)$$

where

Ne = *effective population size*

p_i = the proportional genetic contribution of clone or *genotype* i

p_j = the proportional genetic contribution of *genotype* j

c_{ij} = coancestry between *genotypes* i and j

n = number of *genotypes*

$\mathbf{p}$ = the n x 1 vector of gametic proportions for *genotypes* $i = 1, 2, \ldots, n$

$\mathbf{C}$ = the n x n coancestry matrix for *genotypes* $i = 1, 2, \ldots, n$

The proportional genetic contribution, p_i, of *genotype* i is calculated as follows:

$p_i = f_i/\Sigma f_i$ for proportions based only on samples of female "flower" or cone counts

$p_i = (f_i/\Sigma f_i + m_i/\Sigma m_i)/2$ for proportions based on samples of both female and male "flower" counts

$p_i = n_i/\Sigma n_i$ for proportions based on total counts of cuttings per clone

where

f_i = the number of female "flowers" occurring on *genotype* i (alternatively, cone counts can be used)

m_i = the number of male "flowers" occurring on *genotype* i

n_i = the number of cuttings taken from *genotype* i

Where *genotypes* are unrelated and not inbred, formula (1) simplifies to

$$Ne = 1/\Sigma p_i^2 \qquad (3)$$

COANCESTRIES

Coancestry values for some common relationships between non-inbred individuals are shown below.

Common coancestry values

Relationship between genotypes	Coancestry
Identical (tree with itself or with *ramet* of the same clone)	0.500
Full-sib (two individuals with same mother and father)	0.250
Parent-offspring (individual with mother or with father)	0.250
Half-sib (two individuals with same mother or father but not both; e.g. members of open-pollinated family)	0.125
Unrelated individuals	0.000

CATEGORIES AND CALCULATIONS

Four types of *production facility* are addressed, with a worked example for each.

A. Vegetative production facilities
   1. *stoolbeds* producing vegetative lots of unrelated clones
   2. *stoolbeds* producing vegetative lots of related clones (amplified full-sib or half-sib families)

B. *Seed orchards* including *monoecious* and *dioecious* species
   1. orchards of unrelated and non-inbred *genotypes* (e.g. most first generation clonal orchards, including potted orchards)
   2. orchards of related, non-inbred *genotypes* (e.g. open-pollinated seedling *seed orchards* and advanced generation clonal orchards with related clones)

No example is included of a facility including inbred *genotypes*, since no such facilities are expected in Alberta in the near future. However, such calculations would use equations (1) or (2) with no additional modification.

All calculations for the first and third categories can be done easily in EXCEL, using equation (3). Calculations for most lots from facilities in categories 2 and 4 can be done by means of matrix manipulation using equation (2), in EXCEL; the coancestry matrix need only be constructed once for each facility, and frequency vector **p** reconstructed for each annual *crop*. For *production facilities* including a very large number of *genotypes* (e.g. seedling *seed orchards*), SAS or the ACCESS program noted below can be used.

An ACCESS program developed for calculation of *Ne* for orchards including related *genotypes* using equation (1) was developed by Weyerhaeuser Company, in collaboration with the BC Ministry of Forests; this program is available through the Forest Genetics Program, Alberta Sustainable Resource Development, Edmonton. The contributions of BC Ministry of Forests geneticist Michael Stoehr are gratefully acknowledged.

WORKED EXAMPLES

A. VEGETATIVE MATERIAL

Note: *Ne* calculations for vegetatively reproduced material are based on actual total numbers in a vegetative lot, not on a sample, as for *seed orchards*.

A.1 Vegetative lots of unrelated clones

EXAMPLE 1: A vegetative lot containing 2360 individuals of 10 unrelated clones

Clone	Number of cuttings or plants	p_i	p_i^2
1	300	0.127	0.01616
2	10	0.004	0.00002
3	150	0.064	0.00404
4	240	0.102	0.01034
5	460	0.195	0.03799
6	300	0.127	0.01616
7	190	0.081	0.00648
8	200	0.085	0.00718
9	240	0.102	0.01034
10	270	0.114	0.01309
Total	**2360**		**0.12180**

Using equation (3)

$$\begin{aligned} Ne &= 1/\Sigma p_i^2 \\ &= 1/0.1218 = 8.21 \end{aligned}$$

A.2. Vegetative lots of related clones (amplified full-sib or half-sib families)

This example is worked manually to show the application of equation (1), as well as in matrix notation using equation (2). Calculations for actual vegetative lots would normally be done using matrices in EXCEL or SAS, or by using the ACCESS program available from the Department.

EXAMPLE 2: A vegetative lot containing five clones, with two clones belonging to one full-sib family, and three belonging to a second half-sib family, unrelated to the first family

Coancestry table (showing c_{ij} for each pair of clones i and j)

		Family 1		**Family 2**		
		Clone 1	**2**	**3**	**4**	**5**
Family 1	**Clone 1**	0.5	0.25	0	0	0
	2	0.25	0.5	0	0	0
Family 2	**3**	0	0	0.5	0.125	0.125
	4	0	0	0.125	0.5	0.125
	5	0	0	0.125	0.125	0.5

Clonal frequencies

Family	Clone	Number of cuttings or plants	p_i
1	1	910	0.13
1	2	1960	0.28
2	3	2870	0.41
2	4	1050	0.15
2	5	210	0.03
Total		**7000**	

Construct a weighted table where $x_{ij} = p_i\, p_j\, c_{ij}$

		Family 1		**Family 2**		
		Clone 1	**2**	**3**	**4**	**5**
Family 1	**Clone 1**	0.00845	0.0091	0	0	0
	2	0.0091	0.0392	0	0	0
Family 2	**3**	0	0	0.08405	0.007688	0.001538
	4	0	0	0.007688	0.01125	0.000562
	5	0	0	0.001538	0.000562	0.00045

summing over terms:

$$\Sigma\Sigma p_i\, p_j\, c_{ij} \quad = \quad 0.181175$$

and using equation (1)

$$Ne = \quad 0.5/(\Sigma\Sigma p_i\, p_j\, c_{ij}) \quad = \quad 2.76$$

EXAMPLE 2 reworked using matrices

$$\mathbf{p} = \begin{bmatrix} 0.13 \\ 0.28 \\ 0.41 \\ 0.15 \\ 0.03 \end{bmatrix} \qquad \mathbf{C} = \begin{bmatrix} 0.5 & 0.25 & 0 & 0 & 0 \\ 0.25 & 0.5 & 0 & 0 & 0 \\ 0 & 0 & 0.5 & 0.125 & 0.125 \\ 0 & 0 & 0.125 & 0.5 & 0.125 \\ 0 & 0 & 0.125 & 0.125 & 0.5 \end{bmatrix}$$

$$\mathbf{p'Cp} \quad = \quad 0.181175$$

and using equation (2)

$$Ne \quad = \quad 0.5/\mathbf{p'Cp} \quad = \quad 2.76, \text{ as above.}$$

B. SEED ORCHARD CROPS

(See Appendix 37 for sampling levels required for Ne determination.)

B.1. Seedlots from orchards of unrelated and non-inbred genotypes (e.g. most first generation clonal orchards)

The value of p_i may be calculated using only the female component, i.e. estimates of flower or cone numbers, or using both male and female components, with estimates of pollen cone numbers in addition to estimates of seed cone numbers. In this example we demonstrate both methods.

EXAMPLE 3: A clonal orchard with a total of 50 ramets of 10 clones

Count of female and male "flowers" for each ramet

Clone	Ramet	Females	Males
x123	1	50	500
x123	2	50	600
x123	3	0	100
x123	4	75	660
x123	5	85	1000
x123	6	80	450
x123	7	0	120
x123	8	230	1860
x354	1	0	20
x354	2	0	0
x354	3	25	300
x354	4	0	50
x354	5	0	0
x465	1	50	430
x465	2	350	1980
x466	1	225	2100
x466	2	125	1490
x466	3	425	3580
x466	4	0	0
x466	5	900	7500
x466	6	100	900
x466	7	1450	9800
x466	8	85	400
x487	1	0	50
x487	2	20	200
x487	3	125	980
x487	4	75	640
x699	1	475	3200
x699	2	575	6000
x699	3	275	1300
x699	4	375	2900
x699	5	0	50
x732	1	0	170
x732	2	0	50
x732	3	0	60
x732	4	60	590
x732	5	0	0
x732	6	80	680
x744	1	50	370
x744	2	0	210
x744	3	35	250
x744	4	175	1500
x798	1	225	1900
x798	2	30	290
x798	3	450	5400
x798	4	0	60
x798	5	75	650
x900	1	80	870
x900	2	0	50
x900	3	0	110

Summarize by clone and calculate proportions:

- for proportions based only on female counts: $p_i = f_i/\Sigma f_i$
- for proportions based on both female and male counts: $p_i = (f_i/\Sigma f_i + m_i/\Sigma m_i)/2$

Clone	Ramets	Females (f_i)	Males (m_i)	p_i (f only)	p_i^2 (f only)	p_i (m only)	p_i (m & f)	p_i^2 (m & f)
x123	8	570	5290	0.076	0.006	0.085	0.080	0.006
x354	5	25	370	0.003	0.000	0.006	0.005	0.000
x465	2	400	2410	0.053	0.003	0.039	0.046	0.002
x466	8	3310	25770	0.442	0.196	0.413	0.428	0.183
x487	4	220	1870	0.029	0.001	0.030	0.030	0.001
x699	5	1700	13450	0.227	0.052	0.216	0.221	0.049
x732	6	140	1550	0.019	0.000	0.025	0.022	0.000
x744	4	260	2330	0.035	0.001	0.037	0.036	0.001
x798	5	780	8300	0.104	0.011	0.133	0.119	0.014
x900	3	80	1030	0.011	0.000	0.017	0.014	0.000
Total	50	7485	62370	1.00	0.270	1.00	1.00	0.256
$Ne = 1/\Sigma(p_i^2)$					**3.70400**			**3.906**

In this example, *Ne* based only on female counts = 3.7, while including male counts increases the estimate of *Ne* to 3.91. Including male counts will increase the accuracy of *Ne* estimates, but may result in either increased or decreased *Ne* estimates. Note that *Ne* is considerably less than the number of clones (10). This is due to imbalance in both numbers of *ramets*/clone and in reproductive activity.

B.2. Seedlots from orchards of related, non-inbred genotypes (e.g. open-pollinated seedling seed orchards and advanced generation clonal orchards with related clones)

EXAMPLE 4: a half-sib seedling orchard containing two families with three and two individuals respectively

$$\mathbf{p} = \begin{bmatrix} 0.24 \\ 0.32 \\ 0.09 \\ 0.20 \\ 0.15 \end{bmatrix} \qquad \mathbf{C} = \begin{bmatrix} 0.5 & 0.125 & 0.125 & 0 & 0 \\ 0.125 & 0.5 & 0.125 & 0 & 0 \\ 0.125 & 0.125 & 0.5 & 0 & 0 \\ 0 & 0 & 0 & 0.5 & 0.125 \\ 0 & 0 & 0 & 0.125 & 0.5 \end{bmatrix}$$

$\mathbf{p'Cp} = 0.1546$

and using equation (2)

$Ne = 0.5/\mathbf{p'Cp} = 3.23.$

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Appendix 37. Sampling Levels for Calculation of Ne Values in Orchard Seedlots

See Standards 33.4 and 33.4.1.

Note: These are interim guidelines only. A comprehensive reassessment of sampling requirements should be undertaken once five years of data have been collected.

INTRODUCTION

Effective population size (see Appendix 36 for calculation methods) is used as a surrogate for genetic diversity levels in seed and vegetative lots, and also reflects the degree of imbalance among *genotypes* contributing to a given lot. While genotypic representation in vegetative lots can be readily determined directly, in seed lots this is impossible, and an approximation must be made.

The orchard manager should be aware that *Ne* estimates will vary with the intensity of sampling. These estimates may be considerably lower than, or in some cases higher than, the actual Ne. Estimates based on assessment of only female flowers or cones will be less accurate than those including information from male flowers and reproductive phenology. Since the purpose of *Ne* estimation is to ensure that a threshold has been met, rather than to determine the actual value of Ne, the required intensity of sampling is higher where smaller numbers of *genotypes* contribute.

Simulations with actual orchard data showed that an orchard sample of 10% (as in PSTs) can yield an *Ne* estimate as low as one-fifth of the *Ne* calculated on a 100% orchard survey. On average, the ratio of the *Ne* estimate obtained with 10% sampling to the *Ne* estimate at 100% sampling [Ne(10%)/Ne(100%)] is expected to be approximately 0.5, depending on the distribution of genotypic frequencies. At a 50% sampling intensity, the average Ne(50%)/Ne(100%) ratio increased to approximately 0.9, but may, by chance, be below 0.7. Thus minimum requirements outlined below may not be adequate to demonstrate that *Ne* thresholds have been exceeded. It is the responsibility of the orchard manager to demonstrate, through estimates of gametic contribution, that the minimum required *Ne* has been achieved.

CLONAL SEED ORCHARDS

Table 1 below outlines minimum sampling requirements for clonal *seed orchards.*

Table 1. Sampling requirements for Ne calculations in clonal seed orchards

Clones contributing	Minimum sampling requirement	Genders assessed
100+	PSTs only*	female
75-99	15% including PSTs	male & female
50-74	25% including PSTs	male & female
25-49	50% including PSTs	male & female
< 25	100% - (all trees)	male & female

*PSTs are expected to include at least 10% of orchard trees, to a maximum of 200 PSTs (see Appendix 33).

SEEDLING SEED ORCHARDS

A seedlot from a seedling *seed orchard* containing n families and an average of t trees per family (t>1) can be expected to have a higher *Ne* value than a seedlot from a clonal *seed orchard* with n families and an average of t *ramets* per clone. This is because there is considerable genetic diversity within families, but none within clones. The ratio of the *Ne* from a seedling *seed orchard* with n families to that of a clonal orchard with n clones is independent of n, and increases with increasing t. (See example in Table 2 below.)

Table 2. Ne Comparison: open-pollinated seedling seed orchard with 40 families vs clonal seed orchard with 40 clones*

	Number of Seedlings per Family or Ramets per Clone (t)										
	1	2	3	4	5	6	7	8	9	10	Infinite
Ne of o.p. seedling orchard	40	64	80	91.6	100	106.8	112	116.4	120	123.2	160
Ne of clonal orchard	40	40	40	40	40	40	40	40	40	40	40
Ratio of Ne (seedling orchard) to Ne (clonal orchard)	1.00	1.60	2.00	2.29	2.50	2.67	2.80	2.91	3.00	3.08	4.00

*For simplicity, in this example it is assumed that all clones or families have equal numbers of *ramets* or seedlings, and that all trees are equally productive.

Thus the numbers of trees to be sampled in a seedling *seed orchard* can be lower than in a clonal orchard, for a given number of families or clones.

If the mean family size in the orchard is less than five trees, sampling requirements are as for clonal orchards (Table 3). If the mean family size exceeds five, sampling requirements are given in Table 4.

Table 3. Sampling requirements for Ne calculations in open-pollinated seedling seed orchards with an average of fewer than five trees per family

Families contributing	Minimum sampling requirement	Genders assessed
100+	PSTs only	female
75-99	15% including PSTs	male & female
50-74	25% including PSTs	male & female
25-49	50% including PSTs	male & female
< 25	100% - (all trees)	male & female

Table 4. Sampling requirements for Ne calculations in open-pollinated seedling seed orchards with an average of at least five trees per family

Families contributing	Minimum sampling requirement	Genders assessed
50+	PSTs only	female
37-49	15% including PSTs	male & female
25-36	25% including PSTs	male & female
12-24	50% including PSTs	male & female
< 12	100% - (all trees)	male & female